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_____ Bibliographic

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_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

☒ Other CGN

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Examiner Misook Yu, Ph.D.
703-308-2454 (Phone)
Art Unit 1642
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TYPE OF SEARCH:

NA Sequences: _____
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Full text: _____
Patent Family: _____
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VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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XX WO200166746-A2.
PN
XX
XX 13-SEP-2001.
PD
XX
XX
PF 05-MAR-2001: 2001WO-US07116.
XX
XX
XX 03-MAR-2000: 2000US-0186606.
PR
XX 06-MAR-2000: 2000US-0187247.
PR
XX 06-MAR-2000: 2000US-0187248.
PR
XX 06-MAR-2000: 2000US-0187249.
PR
XX 06-MAR-2000: 2000US-0187250.
PR
XX 06-MAR-2000: 2000US-0187253.
PR
XX 06-MAR-2000: 2000US-0187295.
PR
XX 07-MAR-2000: 2000US-0187296.
PR
XX 21-JUL-2000: 2000US-0219854.
PR
XX 24-JUL-2000: 2000US-0220263.
PR
XX 31-JUL-2000: 2000US-0221942.
PR
XX 21-DEC-2000: 2000US-0257600.
PR
XX 08-JAN-2001: 2001US-0260285.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Padigaru M, Burgess CE, Majumder K, Mishra VS, Li L;
PI Baumgartner JC, Spytek KA, Tchernev VT;
XX
XX MPI: 2001-565586/53.
DR N-PSDB: AAD17016.
XX
XX Novel polypeptides designated as NOVX polypeptides, useful in
PT detection, prevention and treatment of e.g. Parkinson's disease and
PT Cancer -
XX
XX Claim 1: Page 10; 174pp: English.
XX
XX The invention relates to novel G-protein coupled-receptor (GPCR) related
CC polypeptides and their corresponding nucleotides, referred as NOVX or
CC NOV1, NOV2, NOV3, NOV4, NOV5, NOV6, NOV7, NOV8, NOV9 and NOV10. NOVX and
CC its Ab are useful for treating or preventing a NOVX-associated disorder,
CC such as disorder related to cell signal processing and metabolic signal
CC pathway modulation, e.g. diabetes. Pharmaceutical composition comprising
CC NOVX sequence is used to treat or to prevent disorders or syndromes
CC including metabolic disturbances associated with obesity, anorexia,
CC wasting disorders associated with chronic diseases, infectious diseases
CC (particularly infections caused by HIV-1 or HIV-2), cancer-associated
CC cachexia, cancer, Parkinson's disease, Alzheimer's disease, immune
CC disorders, neurodegenerative diseases and haematopoietic disorders. NOVX
CC sequence is also useful for treating developmental diseases, major
CC histocompatibility complex (MHC) II and III diseases (immune diseases),
CC noninsulin-dependent diabetes mellitus (NIDDM1), bulimia, hypotension,
CC acute heart failure, multiple sclerosis, hypertension, osteoporosis,
CC Crohn's disease, Albritght Hereditary Osteodystrophy, angina pectoris,
CC myocardial infarction, asthma, allergies, benign prostatic hypertrophy
CC and psychrotic and neurological disorders, including anxiety, delirium,
CC schizophrenia, manic depression, dementia, severe mental retardation,
CC dentatorubralpallidolysian atrophy (DRPLA) hypophosphataemic rickets,
CC autosomal dominant (2) acrocallosal syndrome and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette syndrome and/or other
CC pathologies. NOVX DNA is used in mapping the chromosomal location of
CC NOVX gene and in forensic biology. The present sequence is GPCR NOV1b
CC protein.
XX
XX Sequence 313 AA:
SQ
Query Match 100.0%; Score 1607; DB 22: Length 313;
Best Local Similarity 100.0%; Pred. No. 4,8e-170;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 FFLTNLSLDLCYTTCTVPQMLVNLCSIRKVISYRGCAQLFTPLALGATEYLLAVMSF 120
DB 61 ffltnslsldlcyttctvpqmlvnlcsirkvisyrgcvaqlfflialgateylllavmsf 120
QY 121 DWFVAICRPLHYSVIMHQRCLDLAAASWTGSSNSWMLSTLRQLPCLCPPIYIDHFLCE 180
DB 121 dwfvaicrplhyshivmhqrcldlaaaswtgssnswwmlstlrqlpclcpipyidhflce 180
QY 181 VPALKLSCVETTANEAELFLVSELFLILPILTLISYAFIVRAVLRIGSAGROKAFGT 240
DB 181 vpalklscvettanearaelflvselflilpiltllisyaflivravlrigsagrqkafgt 240
QY 241 CGSHLIVLSLEFYSTAVSVYLQPPSPSKDGGKMSLEFYGIAPMLNPLVTLRNKEVKEG 300
DB 241 cgsahlivslsfystavsvylqppspskdggkmslffygiapmlnpllytlrnkevkeg 300
QY 301 FKRLLVARVFLIKK 313
DB 301 fkrllvarvflikk 313
RESULT 2
AAU04689
ID AAU04689 standard; Protein; 313 AA.
XX
AC AAU04689;
XX
DT 26-SEP-2001 (first entry)
XX
DE Novel human G-protein coupled receptor (NGPCR).
XX Human: novel G-protein coupled receptor; NGPCR; drug discovery;
KW diagnostic.
XX
XX Homo sapiens.
XX
XX WO200151634-A1.
XX
XX 19-JUL-2001.
XX
XX 05-JAN-2001: 2001WO-US00589.
XX
XX 12-JAN-2000: 2000US-0175764.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Walke DW, Wilganowski NL, Turner CA, Friedrich G, Abuin A;
PI Zambrowicz B, Sands AT;
XX
XX MPI: 2001-442145/47.
DR N-PSDB: AAS08541.
XX
XX New human G protein-coupled receptor and polynucleotides encoding the
PT receptor, useful in identifying, selecting or validating new molecular
PT targets for drug discovery and in diagnostic or prognostic assays -
XX
XX Claim 2: Page 61-62; 65pp: English.
XX
XX The sequence represents the amino acid sequence of novel human G-protein
CC coupled receptor (NGPCR). The NGPCR nucleic acid and protein are useful
CC in identifying, selecting or validating novel molecular targets for drug
CC discovery, as well as in diagnostic or prognostic assays. These are also
CC useful in microarrays or other assay formats, for screening collections
CC of genetic material from patients who have a particular medical condition
CC or for identifying mutations associated with a particular disease.
XX
XX Sequence 313 AA:
SQ
Query Match 99.1%; Score 1593; DB 22: Length 313;
Best Local Similarity 99.7%; Pred. No. 1,7e-168;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MNVWNSDIQEFILLGSDRPWLEFPLLVLVFLISYVTYTGNTLIIIVSRIDTKLHPMY 60
 DB 1 mnvwndsiqefillgfsdrpwlefpilvflisylvtfignltlilivsrldtklhpmy 60
 QY 61 FFLTNLSLDLCYTCVPMQVNLGSIKRVISYRGCAOLFALGATEYLLAVMSF 120
 DB 61 ffltnlsldlcytcvpmqlvnlcsirkvisyrgcvaqlffaalgateyllavmsf 120
 QY 121 DFEVAICRPHYSYIMHQRCLQLAASWVTGFSNSVWLTLLQLPLCDPYVIDHFLCE 180
 DB 121 dfevaicrphysyimhqrclqlaaswvtgfsnswlstdlqlpdcpyvidhflce 180
 QY 181 VPALLKISCVETTANEAELFVSELEFHLIPLTLLISYAFIVRAVLRIQSAEGROKAFGT 240
 DB 181 vpallkiscvettanaeelfvselefhlipltlllisyafivravlrirgsaegrqkafgt 240
 QY 241 CGSHLIYVSLFYSYAVSVLYLOPPSSSKDGKMWSLFYGIITAPMLNPLIYLRKKEVKEG 300
 DB 241 cgsahlivslfysyavsvlylqppspskdgkmwslfygiiapmlnpliyllrnkvekeg 300
 QY 301 FKRLVARVFLIKK 313
 DB 301 fkrivarvflikk 313

RESULT 3
 ID AAG71842 standard; Protein; 313 AA.
 AC AAG71842;
 DT 30-JUL-2001 (first entry)
 DE Human olfactory receptor polypeptide, SEQ ID NO: 1523.
 KW Human: olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation.
 XX Homo sapiens.
 OS
 PN MO200127158-A2.
 PD 19-APR-2001.
 PF 06-OCT-2000; 2000WO-US27582.
 PR 08-OCT-1999; 99US-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 DR MPI; 2001-290713/30.
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 PS Claim 11; Page 972-973; 1857pp; English.
 CC The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful

CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC faculties of different individuals.
 XX

SQ Sequence 313 AA;
 Query Match 99.1%; Score 1593; DB 22; Length 313;
 Best Local Similarity 99.7%; Pred. No. 1,7e-168;
 Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNVWNSDIQEFILLGSDRPWLEFPLLVLVFLISYVTYTGNTLIIIVSRIDTKLHPMY 60
 DB 1 mnvwndsiqefillgfsdrpwlefpilvflisylvtfignltlilivsrldtklhpmy 60
 QY 61 FFLTNLSLDLCYTCVPMQVNLGSIKRVISYRGCAOLFALGATEYLLAVMSF 120
 DB 61 ffltnlsldlcytcvpmqlvnlcsirkvisyrgcvaqlffaalgateyllavmsf 120
 QY 121 DFEVAICRPHYSYIMHQRCLQLAASWVTGFSNSVWLTLLQLPLCDPYVIDHFLCE 180
 DB 121 dfevaicrphysyimhqrclqlaaswvtgfsnswlstdlqlpdcpyvidhflce 180
 QY 181 VPALLKISCVETTANEAELFVSELEFHLIPLTLLISYAFIVRAVLRIQSAEGROKAFGT 240
 DB 181 vpallkiscvettanaeelfvselefhlipltlllisyafivravlrirgsaegrqkafgt 240
 QY 241 CGSHLIYVSLFYSYAVSVLYLOPPSSSKDGKMWSLFYGIITAPMLNPLIYLRKKEVKEG 300
 DB 241 cgsahlivslfysyavsvlylqppspskdgkmwslfygiiapmlnpliyllrnkvekeg 300
 QY 301 FKRLVARVFLIKK 313
 DB 301 fkrivarvflikk 313

RESULT 4
 ID AAE09960 standard; Protein; 313 AA.
 AC AAE09960;
 DT 29-NOV-2001 (first entry)
 DE G-protein coupled-receptor (GPCR) NOVA1 protein.
 KW G-protein coupled-receptor; GPCR; NOVA-associated disorder; obesity;
 KW anorexia; wasting disorder; infection; cachexia; Parkinson's disease;
 KW Alzheimer's disease; immune disorder; neurodegenerative disease; cancer;
 KW anorectic; haematopoietic disorder; major histocompatibility complex;
 KW MHCII; noninsulin-dependent diabetes mellitus; NIDDM; bulimia; asthma;
 KW acute heart failure; hypotension; multiple sclerosis; hypertension;
 KW osteoporosis; Crohn's disease; mental retardation; dementia; allergy;
 KW angina pectoris; myocardial infarction; benign prostatic hypertrophy;
 KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
 KW manic depression; delirium; Alibright Hereditary Osteodystrophy; rickets;
 KW dentatorubropallidolysian atrophy; DRPLA; haemostatic; anticonvulsant;
 KW autosomal dominant (2) acrocallosal syndrome; dyskinesia; neuroleptic;
 KW Huntington's disease; Gilles de la Tourette syndrome; neuroprotective;
 KW neurotropic; antibacterial; protozoacide; fungicide; cytostatic; NOVA1a;
 KW vulnerable; cardiant; osteopathic; antianigmal; anticancer; viroicide;
 KW human immunodeficiency virus; HIV; antidepressant; tranquilliser.
 XX
 OS
 OS
 OS
 FH Key location/Qualifiers
 FT peptide 1..38
 FT /label= signal_peptide
 FT Protein 39..313
 FT /note= "Mature GPCR NOVA1a protein"
 PN MO200166746-A2.
 XX

PD 13-SEP-2001.

XX 05-MAR-2001; 2001MO-US071116.

PF 03-MAR-2000; 2000US-0186606.

XX 06-MAR-2000; 2000US-0187247.

PR 06-MAR-2000; 2000US-0187248.

PR 06-MAR-2000; 2000US-0187249.

PR 06-MAR-2000; 2000US-0187250.

PR 06-MAR-2000; 2000US-0187253.

PR 06-MAR-2000; 2000US-0187295.

PR 06-MAR-2000; 2000US-0187296.

PR 07-MAR-2000; 2000US-0187563.

PR 21-JUL-2000; 2000US-0219854.

PR 24-JUL-2000; 2000US-0220263.

PR 31-JUL-2000; 2000US-0221942.

PR 21-DEC-2000; 2000US-0257600.

PR 08-JAN-2001; 2001US-0260285.

XX (CURA-) CURAGEN CORP.

XX Padigar M, Burgess CE, Majumder K, Mishra VS, Li L;

PI Baumgartner JC, Spytek KA, Tchernev VT;

XX WPI: 2001-565586/63.

DR N-PSDB; AAD17015.

XX Novel polypeptides designated as NOVX polypeptides, useful in

PT detection, prevention and treatment of e.g. Parkinson's disease and

PT Cancer -

PS Claim 1; Page 9; 174pp; English.

XX The invention relates to novel G-protein coupled-receptor (GPCR) related

CC polypeptides and their corresponding nucleotides, referred as NOVX or

CC NOV1, NOV2, NOV3, NOV4, NOV5, NOV6, NOV7, NOV8, NOV9 and NOV10. NOVX or

CC its Ab are useful for treating or preventing a NOVX-associated disorder,

CC such as disorder related to cell signal processing and metabolic signal

CC pathway modulation, e.g. diabetes. Pharmaceutical composition comprising

CC NOVX sequence is used to treat or to prevent disorders or syndromes,

CC including metabolic disturbances associated with obesity, anorexia,

CC wasting disorders associated with chronic diseases, infectious diseases

CC (particularly infections caused by HIV-1 or HIV-2), cancer-associated

CC cachexia, cancer, Parkinson's disease, Alzheimer's disease, immune

CC disorders, neurodegenerative diseases and haematopoietic disorders. NOVX

CC sequence is also useful for treating developmental diseases, major

CC histocompatibility complex (MHC) II and III diseases (immune diseases),

CC noninsulin-dependent diabetes mellitus (NIDDM1), bulimia, hypotension,

CC acute heart failure, multiple sclerosis, hypertension, osteoporosis,

CC Crohn's disease, Albritght Hereditary Osteodystrophy, angina pectoris,

CC myocardial infarction, asthma, allergies, benign prostatic hypertrophy

CC and psychotic and neurological disorders, including anxiety, delirium,

CC schizophrenia, manic depression, dementia, severe mental retardation,

CC dentatorubropallidolusian atrophy (DRPLA) hypophosphataemic rickets,

CC autosomal dominant (2) acrocallosal syndrome and dyskinesias, such as

CC Huntington's disease or Gilles de la Tourette syndrome and/or other

CC pathologies. NOVX DNA is used in mapping the chromosomal location of

CC NOVX gene and in forensic biology. The present sequence is GPCR NOV1a

CC protein.

XX

XX

SO Sequence 313 AA;

Query Match 99.1%; Score 1593; DB 22; Length 313;

Best Local Similarity 99.7%; Pred. No. 1,7e-168;

Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNWVNSIIIOEFILIGSDRPWLEFLLVFLSYTITGNLTIIIVSLRDLTKLHPMY 60

DB 1 MNWVNSIIIOEFILIGSDRPWLEFLLVFLSYTITGNLTIIIVSLRDLTKLHPMY 60

QY 61 FFLTNLSILDLCYTCVPPQMLVNLCSIRKVISYRGCAVOLFPLAIGATEYLLAAVMSF 120

DB 61 ffltnlsildlcytcvppqmlvnlcsirkvisyrgcvaqfflialgateyillavmsf 120

QY 121 DMFVAICRPPLHYSVIMHQRLCLQAAASWYTGFSNSVWLSTLTQLDLPDQRYVIDHEFCE 180

DB 121 drfvaicrplhysvimhqrlclqaaaswytgfsnswlsltlqldpdyidhfe 180

QY 181 VPALKLSQVETTNAAELFLVSELFLHPIPLTLLISAFIVRAVLRIQSGEGQKAFGT 240

DB 181 vpaliklsqvettanaelflvselflhpipltllisafivravlrqsgegrkafgt 240

QY 241 CGSHLIIVWSLFYSTAVSYILOPPSPSSKDGKMYSLFPGIAPMLNPITYLRKKEVKEG 300

DB 241 cgsqliivwslyfstavsyiloppsspskdgkmyslfygiapmlnplylrnkvekeg 300

QY 301 FKRLVAVFLIKK 313

DB 301 fkrivavflikk 313

RESULT 5

AAE09962

ID AAE09962 standard; Protein; 313 AA.

XX

AC AAE09962;

XX

DT 29-NOV-2001 (first entry)

XX

DE G-protein coupled-receptor (GPCR) NOV1c protein.

XX

KW G-protein coupled-receptor; GPCR; NOVX-associated disorder; obesity;

KW anorexia; wasting disorder; infection; cachexia; Parkinson's disease;

KW Alzheimer's disease; immune disorder; neurodegenerative disease; cancer;

KW anorectic; haematopoietic disorder; major histocompatibility complex;

KW MGII; noninsulin-dependent diabetes mellitus; NIDDM1; bulimia; asthma;

KW acute heart failure; hypotension; multiple sclerosis; hypertension;

KW osteoporosis; Crohn's disease; mental retardation; dementia; allergy;

KW angina pectoris; myocardial infarction; benign prostatic hypertrophy;

KW psychotic disorder; neurological disorder; anxiety; schizophrenia;

KW manic depression; delirium; Albritght Hereditary Osteodystrophy; rickets;

KW dentatorubropallidolusian atrophy; DRPLA; haemostatic; anticonvulsant;

KW autosomal dominant (2) acrocallosal syndrome; dyskinesia; neuroleptic;

KW Huntington's disease; Gilles de la Tourette syndrome; neuroprotective;

KW neurotropic; antibacterial; protozoacide; fungicide; cytostatic; NOV1c;

KW vinevarey; cardiant; osteopathic; antitumoral; anticancer; viroicide;

KW human immunodeficiency virus; HIV; antidepressant; tranquilliser.

XX

OS Unidentified.

XX

FT Key location/Qualifiers

FT Peptide 1..38

FT Protein /label= signal_peptide

FT 39..313

PN /note= "Mature GPCR NOV1c protein"

XX

XX WO200166746-A2.

PD 13-SEP-2001.

XX

PF 05-MAR-2001; 2001MO-US071116.

XX

PR 03-MAR-2000; 2000US-0186606.

PR 06-MAR-2000; 2000US-0187247.

PR 06-MAR-2000; 2000US-0187248.

PR 06-MAR-2000; 2000US-0187249.

PR 06-MAR-2000; 2000US-0187250.

PR 06-MAR-2000; 2000US-0187253.

PR 06-MAR-2000; 2000US-0187295.

PR 06-MAR-2000; 2000US-0187296.

PR 07-MAR-2000; 2000US-0187563.

PR 21-JUL-2000; 2000US-0219854.

PR 24-JUL-2000; 2000US-0220263.

PR 31-JUL-2000; 2000US-0221942.

PR 21-DEC-2000; 2000US-0257600.

PR 08-JAN-2001: 2001US-0260285.
 XX (CURA-) CURAGEN CORP.
 XX Padigaru M, Burgess CE, Majumder K, Mishra VS, Li L;
 PI Baumgartner JC, Spytek KA, Tchernev VT;
 XX MPI: 2001-565586/63.
 DR N-PSDB: AAD17017.
 XX Novel polypeptides designated as NOVX polypeptides, useful in
 PT detection, prevention and treatment of e.g. Parkinson's disease and
 PT Cancer -
 XX
 PS Claim 1, Page 12: 174pp: English.
 XX
 XX The invention relates to novel G-protein coupled-receptor (GPCR) related
 CC polypeptides and their corresponding nucleotides, referred as NOVX or
 CC NOV1, NOV2, NOV3, NOV4, NOV5, NOV6, NOV7, NOV8, NOV9 and NOV10. NOVX and
 CC its Ab are useful for treating or preventing a NOVX-associated disorder,
 CC such as disorder related to cell signal processing and metabolic signal
 CC pathway modulation, e.g. diabetes. Pharmaceutical composition comprising
 CC NOVX sequence is used to treat or to prevent disorders or syndromes
 CC including metabolic disturbances associated with obesity, anorexia,
 CC wasting disorders associated with chronic diseases, infectious diseases
 CC (particularly infections caused by HIV-1 or HIV-2), cancer-associated
 CC cachexia, cancer, Parkinson's disease, Alzheimer's disease, immune
 CC disorders, neurodegenerative diseases and haematopoietic disorders. NOVX
 CC sequence is also useful for treating developmental diseases, major
 CC histocompatibility complex (MHC) II and III diseases (immune diseases),
 CC noninsulin-dependent diabetes mellitus (NIDDM1), bulimia, hypotension,
 CC acute heart failure, multiple sclerosis, hypertension, osteoporosis,
 CC Crohn's disease, Alibright Hereditary Osteodystrophy, angina pectoris,
 CC myocardial infarction, asthma, allergies, benign prostatic hypertrophy
 CC and psychotic and neurological disorders, including anxiety, delirium,
 CC schizophrenia, manic depression, dementia, severe mental retardation,
 CC dentatorubralpallidoluysian atrophy (DRPLA) hypophosphataemic rickets,
 CC autosomal dominant (2) acrocallosal syndrome and dyskinesias, such as
 CC Huntington's disease or Gilles de la Tourette syndrome and/or other
 CC pathologies. NOVX DNA is used in mapping the chromosomal location of
 CC NOVX gene and in forensic biology. The present sequence is GPCR NOV1C
 CC protein.
 XX
 XX Sequence 313 AA:
 SO
 Query Match 98.7%; Score 1586; DB 22; Length 313;
 Best Local Similarity 99.0%; Pred. No. 1e-167;
 Matches 310; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
 AAG72915
 ID AAG72915 standard; Protein; 314 AA.
 XX
 XX AAG72915:
 AC
 XX
 DT 30-JUL-2001 (first entry)
 XX
 DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2597.
 XX
 XX Human olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation;
 KW human olfactory receptor data exploratorium; HORDE.
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCT-2000: 2000MO-US27582.
 XX
 PR 08-OCT-1999: 99US-0158615.
 PR 24-FEB-2000: 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PT Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 PI MPI: 2001-290713/30.
 DR
 XX
 XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 XX Example 6; Page 1754-1755; 1857pp: English.
 XX
 XX The present sequence is a polypeptide from the human olfactory receptor
 CC data exploratorium (HORDE). It was used as a query sequence in a database
 CC search of olfactory receptor (OR)-like sequences. The invention relates
 CC to isolated polynucleotides encoding polypeptides involved in olfactory
 CC sensation. The polynucleotides can be used in screening for olfactory
 CC agonists and antagonists. The methods allow for the determination of
 CC primary scents and the identification of the odour receptors used to
 CC detect these primary scents. The methods also enable determination of
 CC secondary scents and the identification of combinations of odour
 CC receptors that are involved in detecting such secondary scents. This
 CC enables the construction of a scent representation (also called a scent
 CC fingerprint or scent profile), which may be used to re-create and edit
 CC scents. Libraries of olfactory receptors are useful for determining the
 CC interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals.
 XX
 XX Sequence 314 AA:
 SO
 Query Match 81.9%; Score 1316; DB 22; Length 314;
 Best Local Similarity 81.8%; Pred. No. 1.e-137;
 Matches 256; Conservative 25; Mismatches 32; Indels 0; Gaps 0;

```

Db      122 drvaicrphylsilmqricfglaaswsgfnsvglstwtlkmplcgkhkevdfhfc 181
QY      181 VPAALKISCVEETANAEALFLVSELPFLIPLTLISYAFIVRAVLRIOGAEGROKAFGT 240
Db      182 vpaalkiscvdtaneaeelffivfillpvtlllisyafivagvirigaegrkafgt 241
QY      241 CGSHLIVSLFYSTAVSVYLQPPSPSSKDGKMYSLFYGIAPMLNPLIYTLRNKEVEKG 300
Db      242 cgsahlivslfygtalsmylqppspsskdrqkmvslfcgllapmlnpllytlrnkvekea 301
QY      301 FKRUVARVFLIKK 313
Db      302 fkrllqrvflikk 314

RESULT 7
AAG71493
ID      AAG71493 standard; Protein; 357 AA.
XX
AC      AAG71493;
XX
DT      30-JUL-2001 (first entry)
XX
DE      Human olfactory receptor polypeptide, SEQ ID NO: 1174.
XX
KW      Human; olfactory receptor; OR; primary scent determination;
KM      secondary scent determination; polypeptide library; odour receptor;
XX      scent profile; scent fingerprint; scent representation.
XX
OS      Homo sapiens.
XX
PN      WO200127158-A2.
XX
PD      19-APR-2001.
XX
PE      06-OCT-2000; 2000MO-US27582.
XX
PR      08-OCT-1999; 99US-0158615.
XX
PR      24-FEB-2000; 2000US-0184809.
XX
PA      (DIGI-) DIGISCENTS.
XX      (YEDA ) YEDA RES & DEV CO LTD.
XX
PI      Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR      WPI; 2001-290713/30.
XX
PT      New polynucleotides which encode polypeptides involved in olfactory
XX      sensation for identifying olfactory agonists and antagonists -
XX
PS      Claim 11; Page 690-691; 1857pp; English.
XX
CC      The present sequence is an olfactory receptor which is encoded by
CC      one of a number of novel polynucleotides. The polynucleotides can be
CC      used in screening for olfactory agonists and antagonists. The methods
CC      allow for the determination of primary scents and the identification
CC      of the odour receptors used to detect these primary scents. The methods
CC      also enable determination of secondary scents and the identification of
CC      combinations of odour receptors that are involved in detecting such
CC      secondary scents. This enables the construction of a scent representation
CC      (also called a scent fingerprint or scent profile), which may be used to
CC      re-create and edit scents. Libraries of olfactory receptors are useful
CC      for determining the interaction pattern of a composition with the
CC      receptors, and can be used for determining differences in the olfactory
CC      faculties of different individuals.
XX
SQ      Sequence 357 AA;

```

```

Query Match      80.6%; Score 1295; DB 22; Length 357;
Best Local Similarity 81.3%; Pred. No. 2.7e-135;
Matches 252; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

```

```

QY      1 MNWVNDIIIOEFLIGSDRPMLEFPLLVYELLISYTVIFGNLTIIIVSRUDTFLHTPMY 60
Db      1 mnwvnxkvpgefilllvdsdpwleiprfvmflfsgyllitfgnltllvshvdfllhpm 60
QY      61 FFLTNLSLDLCYTTCYTPQMLVNLCSIRKVISYRGCAQLFPLGATEYLLAVMSF 120
Db      61 ffltnslldlcytstevpmqlvnlcntrkvisyrgvcaqlfflaigsteclllavmcf 120
QY      121 DMFAIIRPHIYSYIMIORCLQLAASWYTGPSNSWLSSTLTLQDLCPYVDHDLCE 180
Db      121 drvaicrphylsilmqricfglaaswsgfnsvglstwtlkmplcgkhkevdfhfc 180
QY      181 VPAALKISCVEETANAEALFLVSELPFLIPLTLISYAFIVRAVLRIOGAEGROKAFGT 240
Db      181 vpaalkiscvdtaneaeelffivfillpvtlllisyafivagvirigaegrkafgt 240
QY      241 CGSHLIVSLFYSTAVSVYLQPPSPSSKDGKMYSLFYGIAPMLNPLIYTLRNKEVEKG 300
Db      241 cgsahlivslfygtalsmylqppspsskdrqkmvslfcgllapmlnpllytlrnkvekea 300
QY      301 FKRUVARVFL 310
Db      301 fkrivaksll 310

```

```

RESULT 8
AAG72074
ID      AAG72074 standard; Protein; 357 AA.
XX
AC      AAG72074;
XX
DT      30-JUL-2001 (first entry)
XX
DE      Human olfactory receptor polypeptide, SEQ ID NO: 1755.
XX
KW      Human; olfactory receptor; OR; primary scent determination;
KM      secondary scent determination; polypeptide library; odour receptor;
XX      scent profile; scent fingerprint; scent representation.
XX
OS      Homo sapiens.
XX
PN      WO200127158-A2.
XX
PD      19-APR-2001.
XX
PE      06-OCT-2000; 2000MO-US27582.
XX
PR      08-OCT-1999; 99US-0158615.
XX
PR      24-FEB-2000; 2000US-0184809.
XX
PA      (DIGI-) DIGISCENTS.
XX      (YEDA ) YEDA RES & DEV CO LTD.
XX
PI      Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX
DR      WPI; 2001-290713/30.
XX
PT      New polynucleotides which encode polypeptides involved in olfactory
XX      sensation for identifying olfactory agonists and antagonists -
XX
PS      Claim 11; Page 1150-1151; 1857pp; English.
XX
CC      The present sequence is an olfactory receptor which is encoded by
CC      one of a number of novel polynucleotides. The polynucleotides can be
CC      used in screening for olfactory agonists and antagonists. The methods
CC      allow for the determination of primary scents and the identification
CC      of the odour receptors used to detect these primary scents. The methods
CC      also enable determination of secondary scents and the identification of
CC      combinations of odour receptors that are involved in detecting such
CC      secondary scents. This enables the construction of a scent representation
CC      (also called a scent fingerprint or scent profile), which may be used to
CC      re-create and edit scents. Libraries of olfactory receptors are useful

```

SQ Sequence 357 AA;

Matches 252; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

61 FELTNSLLDLCYTTCTVPQMLVNLCSIRKVISYRGVAQLFELALGATEYLLAVMSF 120

Db 121 drfvaicrplhyslimbqrlcfqlaaswisgfsnsvlqstwtlkmplcgkhkevdfce 180

QY 241 CGSHLIVSLFYSTAVSVYLQPPSPSSKDQGMVSLFYGIAPMLNPLITYTLRNKEVKEG 300

Db 301 fkrivaks11 310 .

ID AAG73003 standard; Protein; 313 AA.

KW scent profile; scent fingerprint; scent representation.

PN W0200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

XX XX

PA (YEDA) YEDA RES & DEV CO LTD.

PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory

PS Example 6; Page 1815; 1857pp; English

XX

cc individuals.

```

      Local Similarity: 70.00%, Freq: NO: 2:35 131,
Matches: 244; Conservative: 29; Mismatches: 40; Indels: 0; Gaps: 0;

```

[illegible]

Db 181 vpa1klscvdtaneaelffisvlllpvtlllisyafivqavlkirsacrkaftg 240

XX

XX 3
* 3
C 3
E 3
F 3
C 3

[illegible]

XX

secondary scent determination; polypeptide library; odour receptor, KW

KW human olfactory receptor data exploratorium; HORDE

OS Homo sapiens.

PN W0200127158-A2

PD 19-APR-2001.

XX

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.
 XX (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX WPI; 2001-290713/30.
 DR
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 PS Example 6; Page 1755; 1857pp; English.
 XX
 CC The present sequence is a polypeptide from the human olfactory receptor
 CC data exploratorium (HOREDE). It was used as a query sequence in a database
 CC search of olfactory receptor (OR)-like sequences. The invention relates
 CC to isolated polynucleotides encoding polypeptides involved in olfactory
 CC sensation. The polynucleotides can be used in screening for olfactory
 CC agonists and antagonists. The methods allow for the determination of
 CC primary scents and the identification of the odour receptors used to
 CC detect these primary scents. The methods also enable determination of
 CC secondary scents and the identification of combinations of odour
 CC receptors that are involved in detecting such secondary scents. This
 CC enables the construction of a scent representation (also called a scent
 CC fingerprint or scent profile), which may be used to re-create and edit
 CC scents. Libraries of olfactory receptors are useful for determining the
 CC interaction pattern of a composition with the receptors, and can be
 CC used for determining differences in the olfactory faculties of different
 CC individuals.
 XX
 SQ Sequence 343 AA;

Query Match 78.3%; Score 1259; DB 22; Length 343;
 Best Local Similarity 78.0%; Pred. No. 2.6e-131;
 Matches 244; Conservative 29; Mismatches 40; Indels 0; Gaps 0;

QY 1 MNWVNDSTIOEFILGFSRPMLEFPLLYVFLSYVTITGNLTILVSRDTHPTMY 60
 DB 5 msvenesistreflllgfsdrpwlplfvfvlvysyaltifgmmlllvsrdscklhpmy 64
 QY 61 FELTNLSLIDLCYTCVPOMLVNLGSRKRVYSRGCVAQIFILAGPEYLLAAWSF 120
 DB 65 flfnlsldcyltsrvpqlmlncstrkvisygcvgvqflfllsgstecfllyvmsl 124
 QY 121 DMEVAICRPVHYSYMQRCLQLAASWVTFGSNSWMLSTLTQLPCDPYVIDHFCE 180
 DB 125 drfaicrplhyrlymqrclhaaacwlsfgnsylvgtwltqmpicgkvdhffice 184
 QY 181 VPALKLSVETTANAEALFLVSELPHLIPFTLILISYAFIVRAVLRIQSAEGRQAKGT 240
 DB 185 vpalklsicvdtaneaelffisvllfllpytlilisyafivgvlktrsecrrkafgt 244
 QY 241 CGSLHLYVSLFYTRAVSVYIQPPSPSSKDGKMSLFYGIAPMLNPLITLRKKEVKEG 300
 DB 245 cgsllhlyvslfytravslmylqppspsskdgkmslyfgyitlpmlnplylrneevkga 304
 QY 301 FKRLVAVPLIRK 313
 DB 305 fkrilmkrlililgk 317

RESULT 11
 AAB43266
 ID AAB43266 standard; Protein; 313 AA.
 AC AAB43266;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF3030 polypeptide sequence SEQ ID NO: 6060.
 XX

KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnery; antipsoptic; antiparkinsonian; nootropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiparkinsonian; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal hemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 KW
 XX Homo sapiens.
 OS
 XX
 PN W0200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2000-602362/57.
 DR N-PSDB; AAC77475.
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 XX Claim 11; Page 5246-5247; 5507pp; English.
 PS
 CC AAC74446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
 CC antipsoptic; antiparkinsonian; nootropic; neuroprotective;
 CC anticonvulsant; osteopathic; antiparkinsonian; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal hemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 XX
 SQ Sequence 313 AA;

Query Match 70.3%; Score 1130; DB 21; Length 313;
 Best Local Similarity 70.3%; Pred. No. 5e-117;
 Matches 220; Conservative 34; Mismatches 59; Indels 0; Gaps 0;

QY 1 MNWVNDSTIOEFILGFSRPMLEFPLLYVFLSYVTITGNLTILVSRDTHPTMY 60
 DB 1 mnwvnsdpkfeilllgfsdrpwlplfvfvlvysyaltifgmmlllvsrdscklhpmy 60

XX 08-OCT-1999; 9905-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 XX (YEDA) YEDA RES & DEV CO LTD.
 PI Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I;
 XX WPI; 2001-290713/30.
 DR
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 PS Claim 11; Page 1136-1137; 1857pp; English.
 XX
 CC The present sequence is an olfactory receptor which is encoded by
 CC one of a number of novel polynucleotides. The polynucleotides can be
 CC used in screening for olfactory agonists and antagonists. The methods
 CC allow for the determination of primary scents and the identification
 CC of the odour receptors used to detect these primary scents. The methods
 CC also enable determination of secondary scents and the identification of
 CC combinations of odour receptors that are involved in detecting such
 CC secondary scents. This enables the construction of a scent representation
 CC (also called a scent fingerprint or scent profile), which may be used to
 CC re-create and edit scents. Libraries of olfactory receptors are useful
 CC for determining the interaction pattern of a composition with the
 CC receptors, and can be used for determining differences in the olfactory
 CC faculties of different individuals.
 XX
 SO Sequence 216 AA;

Query Match 66.9%; Score 1075; DB 22; Length 216;
 Best Local Similarity 98.6%; Pred. No. 4e-111;
 Matches 213; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 68 LLDCTTCYTPQMLVNICIRKVIYIRGCYAOLEFIPALGATEYLLIAMSFDMEVAIC 127
 |||||||
 Db 1 lldcyttctcpqmlvnicirkyisyrvcvqgllfflalgatgylilavmsfdrfvaic 60
 |||||||

QY 128 RPLHYSVIMHORLCLQIAAASWMTGFNSVWLSLTLOPLCDPYVIDHFIQCEVPALIKL 187
 |||||||
 Db 61 rplhyssvmhgrlclqlaasrvcgfsnswlscldqldpcdpyvidhfiqcevpallkl 120
 |||||||

QY 188 SCVETTANAEELFVSELFHPLPLTLILISYAFIVRAVLRIQSAEGRQKAFGCGSHLIV 247
 |||||||
 Db 121 scvettaneaelflvselfhplpltlilisyafivravlrirqsaegrqkafgctgshliv 180
 |||||||

QY 248 VSLFYSTRVSYRLQPPSPSSKDQGMWSLFYGIAP 283
 |||||
 Db 181 vslnstlsvsvylqppspsskdqgkmwslfygiap 216
 |||||

Search completed: August 25, 2002, 20:07:13
 Job time: 4206 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2002, 18:57:37 ; Search time 32.69 Seconds

(without alignments)
233.870 Million cell updates/sec

Title: US-09-800-321a-4

Perfect score: 1607

Sequence: 1 MNWVDSIIQEFILIGFSDR.....NKEVGEGRRLVAVFLINK 313

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents .AA:*
1: /cgn2_6/prodata/2/1aa/5a_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5b_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6a_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6b_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	691	43.0	309	3 US-08-988-876-5	Sequence 5, Appl1
2	655	40.8	314	3 US-08-988-876-7	Sequence 7, Appl1
3	654.5	40.7	321	4 US-08-748-506-18	Sequence 18, Appl1
4	651.5	40.5	321	4 US-08-748-506-10	Sequence 10, Appl1
5	647.5	40.3	321	4 US-08-748-506-20	Sequence 20, Appl1
6	645	40.1	333	3 US-08-988-876-6	Sequence 6, Appl1
7	644.5	40.1	321	4 US-08-748-506-12	Sequence 12, Appl1
8	640	39.8	316	2 US-08-827-291A-2	Sequence 2, Appl1
9	638.5	39.7	321	4 US-08-748-506-13	Sequence 13, Appl1
10	630.5	39.2	321	4 US-08-748-506-19	Sequence 19, Appl1
11	628.5	39.1	321	4 US-08-748-506-11	Sequence 11, Appl1
12	622.5	38.7	236	2 US-08-467-948A-2	Sequence 2, Appl1
13	622.5	38.7	236	3 US-08-467-947A-2	Sequence 2, Appl1
14	596	37.1	284	1 US-08-118-270-61	Sequence 61, Appl1
15	596	37.1	284	5 PCT-US93-08528-61	Sequence 61, Appl1
16	589	36.7	327	4 US-08-748-506-24	Sequence 24, Appl1
17	589	36.7	327	4 US-08-748-506-22	Sequence 22, Appl1
18	589	36.7	327	4 US-08-748-506-23	Sequence 23, Appl1
19	579	36.0	327	4 US-08-748-506-14	Sequence 14, Appl1
20	572.5	35.6	284	1 US-08-118-270-67	Sequence 67, Appl1
21	572.5	35.6	284	5 PCT-US93-08528-67	Sequence 67, Appl1
22	548.5	34.1	293	1 US-08-118-270-60	Sequence 60, Appl1
23	548.5	34.1	293	5 PCT-US93-08528-60	Sequence 60, Appl1
24	548	34.1	247	1 US-08-465-980-3	Sequence 3, Appl1
25	548	34.1	247	2 US-09-053-303-3	Sequence 3, Appl1
26	548	34.1	247	5 PCT-US95-07093-3	Sequence 3, Appl1
27	546	34.0	277	1 US-08-118-270-62	Sequence 62, Appl1

28	546	34.0	227	5 PCT-US93-08528-62	Sequence 62, Appl1
29	529.5	32.9	286	1 US-08-118-270-65	Sequence 65, Appl1
30	529.5	32.9	286	5 PCT-US93-08528-65	Sequence 65, Appl1
31	526	32.7	273	1 US-08-118-270-63	Sequence 63, Appl1
32	526	32.7	273	5 PCT-US93-08528-63	Sequence 63, Appl1
33	525	32.7	275	1 US-08-118-270-66	Sequence 66, Appl1
34	525	32.7	275	5 PCT-US93-08528-66	Sequence 66, Appl1
35	522	32.5	277	1 US-08-118-270-68	Sequence 68, Appl1
36	522	32.5	277	5 PCT-US93-08528-68	Sequence 68, Appl1
37	520	32.4	222	2 US-08-467-948A-27	Sequence 27, Appl1
38	520	32.4	222	3 US-08-467-947A-27	Sequence 27, Appl1
39	519.5	32.3	274	1 US-08-118-270-69	Sequence 69, Appl1
40	519.5	32.3	274	5 PCT-US93-08528-69	Sequence 69, Appl1
41	519	32.3	269	1 US-08-118-270-64	Sequence 64, Appl1
42	519	32.3	269	5 PCT-US93-08528-64	Sequence 64, Appl1
43	393	24.5	320	4 US-09-439-313-527	Sequence 527, Appl1
44	377	23.5	320	1 US-08-465-980-2	Sequence 2, Appl1
45	377	23.5	320	2 US-09-053-303-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-08-988-876-5
Sequence 5, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION/DOCKET NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1314667
US-08-988-876-5

[illegible]

```

1      RESULT 2
2      US-08-988-876-7
3      : Sequence 7, Application US/08988876
4      : Patent No. 6063596
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Lal, Preeti
9      : APPLICANT: Bandman, Olga
10     : APPLICANT: Hillman, Jennifer L.
11     : APPLICANT: Yue, Henry
12     : TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
13     : TITLE OF INVENTION: WITH IMMUNE RESPONSE
14     : NUMBER OF SEQUENCES: 9
15     : CORRESPONDENCE ADDRESS:
16     : ADDRESSEE: Inocyte Pharmaceuticals, Inc.
17     : STREET: 3174 Porter Drive
18     : CITY: Palo Alto
19     : STATE: CA
20     : COUNTRY: USA
21     : ZIP: 94304
22     :
23     : COMPUTER READABLE FORM:
24     : MEDIUM TYPE: Diskette
25     : COMPUTER: IBM Compatible
26     : OPERATING SYSTEM: DOS
27     : SOFTWARE: FASTSEQ for Windows Version 2.0
28     :
29     : CURRENT APPLICATION DATA:
30     : APPLICATION NUMBER: US/08/988,876
31     : FILING DATE: Herewith
32     : CLASSIFICATION:
33     :
34     : PRIOR APPLICATION DATA:
35     : APPLICATION NUMBER:
36     : FILING DATE:
37     :
38     : ATTORNEY/AGENT INFORMATION:
39     : NAME: Billings, Lucy J.
40     : REGISTRATION NUMBER: 36,749
41     : REFERENCE/DOCKET NUMBER: PF-0441 US
42     : TELECOMMUNICATION INFORMATION:
43     : TELEPHONE: 650-855-0555
44     : TELEFAX: 650-845-4166
45     :
46     : TELEX:
47     :
48     : INFORMATION FOR SEQ ID NO: 7:
49     :
50     : SEQUENCE CHARACTERISTICS:
51     : LENGTH: 314 amino acids
52     : TYPE: amino acid
53     : STRANDEDNESS: single
54     : TOPOLOGY: linear
55     :
56     : IMMEDIATE SOURCE:
57     : LIBRARY: GenBank

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CLONE: 32086
US-08-988-876-7

Query Match	40.8%;	Score 655;	DB 3;	Length 314;
Best Local Similarity	43.5%;	Pred. No. 2.2e-50;		
Matches 131;	Conservative 61;	Mismatches 109;	Indels 0;	Gaps 0;

[illegible]

```

1      RESULT 3
2      US-08-748-506-18
3      Sequence 18, Application US/08748506
4      Patent No. 6139707
5      GENERAL INFORMATION:
6      APPLICANT: Ronnett et al.
7      TITLE OF INVENTION: NOVEL SPERM RECEPTORS
8      NUMBER OF SEQUENCES: 31
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Leydig, Volt & Mayer, Ltd.
11     STREET: Two Prudential Plaza, Suite 4900
12     CITY: Chicago
13     STATE: IL
14     COUNTRY: US
15     ZIP: 60601-6780
16     COMPUTER READABLE FORM:
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC-DOS/MS-DOS
20     SOFTWARE: PatentIn Release #1.0, Version #1.23
21     CURRENT APPLICATION DATA:
22     APPLICATION NUMBER: US/08/748,506
23     FILING DATE: 08-NOV-1996
24     CLASSIFICATION: 435
25     PRIOR APPLICATION DATA:
26     APPLICATION NUMBER: US 60/033,751
27     FILING DATE: 09-NOV-1995
28     CLASSIFICATION: 435
29     ATTORNEY/AGENT INFORMATION:
30     REFERENCE/DOCKET NUMBER: 74940
31     TELECOMMUNICATION INFORMATION:
32     TELEPHONE: 312-616-5600
33     TELEFAX: 312-616-5700
34     INFORMATION FOR SEQ ID NO: 18:
35     SEQUENCE CHARACTERISTICS:
36     LENGTH: 321 amino acids
37     TYPE: amino acid
38     TOPOLOGY: unknown
39     MOLECULE TYPE: protein
40     US-08-748-506-18

```

```

Query Match          40.7%; Score 654.5; DB 4; Length 321;
Best Local Similarity 44.7%; Pred. NO. 2.5e-50;
Matches 135; Conservative 48; Mismatches 118; Indels 1; Gaps 1;

QY      3  WVNNSI-IOEPIILLGSGSPRMLEFPLVAVPLISYVTITFGNLTILVSRDLTKLTPMYE 61
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
Db      8  WQENSLVYKHKFAFKFSSEVPGECEFLIFMLILMLPLVSLGNIILVLAICTSLSLTPMYF 67
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
QY      62  FLNLSLIDLCYTTCTVBPQMLVNLCSIRKVISYRCVAQLFFIALGATEYLLAVMSFD 121
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
Db      68  FLNLSLIEIYGTCSVYIPKMLQSLVSEAREISREGCATQMFEEFAFFGITECCLAMAFD 127
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
QY      122  MFWANICRPLHYSVIMHQAQLQLAASAVYGFNSVMLSTLTQLPLCDPYIYIDHFLCEV 181
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
Db      128  RCMACISPLHATYRSTRREVCAHLAIVSGMCCIVSLGQTNLFISLNFPGPCIDHFFCDL 187
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
QY      182  PALKLSCVETTANEAELFVSELFHLIPLILISYAFIYAVADRIQSAEGROKAFGTC 241
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
Db      188  PPLALACGDIQSQNAALFVYAVLCLISSPFLIILISYKILAVILMSPERHKAHLSIC 247
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
QY      242  GSHLIVLEFYSYAVSVYLPPSPSSKQDGKMSVLEFYGIAPMLNPLIYTLNKEVKEGF 301
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
Db      248  SSHLVVLTLEFYGSACITFLRPKSSHSHPQMDKFLALFYVYVSMNPILYSLNKKEVKAAL 307
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
QY      302  KR 303
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111
Db      308  RR 309
      1  : : : : : 11 : : : : : 1 : : : : : 11 : : : : : 111111

RESULT      4
US-08-748-506-10
: Sequence 10, Application US/08748506
: Patent No. 6159707
: GENERAL INFORMATION:
: APPLICANT: Ronnett et al.
: TITLE OF INVENTION: NOVEL SPERM RECEPTORS
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Leydig, Volt & Mayer, Ltd.
: STREET: Two Prudential Plaza, Suite 4900
: CITY: Chicago
: STATE: IL
: COUNTRY: US
: ZIP: 60601-6780
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/748,506
: FILING DATE: 08-NOV-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/033,751
: FILING DATE: 09-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: REFERENCE/DOCKET NUMBER: 74940
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5600
: TELEFAX: 312-616-5700
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 321 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-748-506-10

```

	Query Match	Similarity	40.5%	Score	651.5	DB	4	Length	321
	Best Local	Similarity	44.7%	Pred.	No.	4,6e-50			
	Matches	135	Conservative	47	Mismatches	119	Indels	1	Gaps
QY	3	WVNDSI	-IQEFLILGFSDRPWLEFPPLLVLFLLISYTVITFGNLTITILVSRDLKRLTPMYE	61					
Db	8	WOENSLITVKKHFAFAKFESEVPGCEFLFNLLIMFLMFLSILGNTLIVLALITSPSLHMPMF	67						
QY	62	FLTNLSLIDICTCTCTVPMQVLNCSIRKVISYRCVCVQLFELMALGATEYILLAMSPD	121						
Db	68	FLANLSLEIGTCSVIPIMQSLVSEAEKLSRECCATQMEFFAFRGITTECLLAMAPD	127						
QY	122	WFAVACRPLHYSVINHQRCQLQALAASWVTGFSNSVWLSTLTLQLPLCDPYVIDHFLCEY	181						
Db	128	RCMAICSPLRHATRMSREVCANHLAVSMQMGCVISLQGNPFILSNFCGCPCEIDHFQDL	187						
QY	182	PALKLSCVETTANAELEFVSEHLHLPLTILISYAFIYAAYLRIGQAEGRQKAFGC	241						
Db	188	PPLALAGDTSQNSNAIAFVAVAVLCITSSPELLITISYVLLILAVLMLSPDEBRHRLASTC	247						
QY	242	GSHLIVSLFYSTAVSYLQPPSPSSKDDGKMWSLFYGIAPMLNPILYTLRNKEVEKEGF	301						
Db	248	SSHLLVTLFLFGSACITLYLRKSSSHSPGMDKRLALEFYTVYVTSMLNPITYISLNKREVKAL	307						
QY	302	KR	303						
Db	308	RR	309						

RESULT 5
 US-08-748-506-20
 Sequence 20 Application US/08748506
 Patent No. 6159707
 GENERAL INFORMATION:
 APPLICANT: Romnett et al.
 TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Volt & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 CITY: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,506
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,751
 FILING DATE: 09-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION: 74940
 REFERENCE/DOCKET NUMBER:
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5700
 TELEFAX: 312-616-5600
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-748-506-20

Best Local Similarity 42.7%; Pred. No. 1e-49;
Matches 134; Conservative 56; Mismatches 121; Indels 3; Gaps 2

[illegible]

RESULT 6
US-08-988-876-6

```

1      GENERAL INFORMATION:
2      APPLICANT: Lal, Preeti
3      APPLICANT: Bandman, Olga
4      APPLICANT: Hillman, Jennifer L.
5      APPLICANT: Yue, Henry
6      TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
7      TITLE OF INVENTION: WITH IMMUNE RESPONSE
8      NUMBER OF SEQUENCES: 9
9      CORRESPONDENCE ADDRESS:
10     ADDRESSEE: Incyte Pharmaceuticals, Inc.
11     STREET: 3174 Porter Drive
12     CITY: Palo Alto
13     STATE: CA
14     COUNTRY: USA
15     ZIP: 94304
16
17     COMPUTER READABLE FORM:
18     MEDIUM TYPE: Diskette
19     COMPUTER: IBM Compatible
20     OPERATING SYSTEM: DOS
21     SOFTWARE: FastSeq for Windows Version 2.0
22
23     CURRENT APPLICATION DATA:
24     APPLICATION NUMBER: US/08/988,876
25     FILING DATE: Herewith
26
27     CLASSIFICATION:
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER:
30     FILING DATE:
31
32     ATTORNEY/AGENT INFORMATION:
33     NAME: Billings, Lucy J.
34     REGISTRATION NUMBER: 36,749
35     REFERENCE/DOCKET NUMBER: PF-0441 US
36
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: 650-855-0555
39     TELEFAX: 650-845-4166
40
41     TELEX:
42
43     INFORMATION FOR SEQ ID NO: 6:
44     SEQUENCE CHARACTERISTICS:
45     LENGTH: 333 amino acids
46     TYPE: amino acid
47     STRANDEDNESS: single
48     TOPOLOGY: linear
49

```

;
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 205814
US-08-988-876-6

Query Match	40.1%	Score 645	DB 3	Length 333
Best Local Similarity	40.9%	Pred NO. 1.8e-49		
Matches 124	Conservative 62	Mismatches 117	Indels 0	Gaps 0

[illegible]

RESULT 7
US-08-748-506-12

```

1  GENERAL INFORMATION:
2  APPLICANT: Ronnett et al.
3  TITLE OF INVENTION: NOVEL SPERM RECEPTORS
4  NUMBER OF SEQUENCES: 31
5  CORRESPONDENCE ADDRESS:
6  ADDRESSEE: Leydig, Volt & Mayer, Ltd.
7  STREET: Two Prudential Plaza, Suite 4900
8  CITY: Chicago
9  STATE: IL
10 COUNTRY: US
11 ZIP: 60601-6780
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/748,506
19 FILING DATE: 08-NOV-1996
20 CLASSIFICATION: 435
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 60/033,751
23 FILING DATE: 09-NOV-1995
24 CLASSIFICATION: 435
25 ATTORNEY/AGENT INFORMATION:
26 REFERENCE/DOCKET NUMBER: 74940
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 312-616-5600
29 TELEFAX: 312-616-5700
30 INFORMATION FOR SEQ ID NO: 12:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 321 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear

```


MOLECULE TYPE: protein
US-08-748-506-12

Query Match	40.1%;	Score 644.5;	DB 4;	Length 321;
Best Local Similarity	-42.7%;	Pred. No. 1.9e-49;		
Matches 134; Conservative	55;	Mismatches 122;	Indels 3;	Gaps 2;

```

QY 3 WVNDSI--IOEIIILGFGDRPLMEPLLVLFISTVYIFENLNTIIVSRDITKLHPMPYE 61
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 8 WQENSLSVKRPAPKAFKSEVGECEFLTLLTLLHMFVSLTGQWTLALACTSPSLHMPYF 67
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 62 FLTMIISLLDCYTCYCPOMLVNLCISIRKYSYRGCAOLFIFALGATEYELLAAMSPD 121
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 68 FLALSLLEIGYTCYSVIPKMQISLVSRARGISWEGCASQMFPLFBSITCCLLAAMAFD 127
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 122 WFAVACRPLHYSVIMHORCLQLQALAAASWYGFNSVNLSTLTQLPLCDPEYVIDHFLCEY 181
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 128 RYMAICSPPLHATMRMSGVCAYLAIYSWMGCIYGLQGTNFIISLNRGCEIDHFFCDL 187
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 182 PALLKLSCEVTANEAELFLVSELFIHLIPLTLILISTAYFRAVLRIQSAEGRQKAGTVC 241
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 188 PRLTALACGPTSONEAFIIVAAYVLCIFSPPELLIISTSVRIIVAVLWMPSEGRHKLALSTC 247
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 242 GSHLIIVSLFYSYRAVSYYLQPPSPSSKQDGKAMSLFEGITAIAMPNLITLYLRNKEVEGF 301
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 248 SSHLLVLTFLFYGSYSAIYLRKSSSHSPGVCKLALFYTSTSMLPITYELRNKEVYGAL 307
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 302 KRLVA--RVFLIK 313
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 308 KRIGLKKVLTMR 321
    | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

RESULT 28
 US-08-827-291A-2
 Sequence 2, Application US/08827291A
 Patent No. 5874243
 GENERAL INFORMATION:
 APPLICANT: Macina, Roberto
 APPLICANT: Sathe, Ganesh
 TITLE OF INVENTION: NOVEL OLRCL5 RECEPTOR
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY:
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/827,291A
 FILING DATE: 28-MAR-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: King, William T
 REGISTRATION NUMBER: 30,954
 REFERENCE/DOCKET NUMBER: GP50001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5015
 TELEFAX: 610-270-5090
 TELEX:
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 316 amino acids
 TYPE: amino acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-827-291A-2

```

[illegible]

US-08-748-506-13
 9
 Sequence 13, Application US/08748506
 Patent No. 6135707
 GENERAL INFORMATION:
 APPLICANT: Ronnett et al.
 TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 NUMBER OF SEQUENCES: 31
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Leydig, Volt & Mayer, Ltd.
 STREET: Two Prudential Plaza, Suite 4900
 City: Chicago
 STATE: IL
 COUNTRY: US
 ZIP: 60601-6780
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/748,506
 FILING DATE: 08-NOV-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/033,751
 FILING DATE: 09-NOV-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 REFERENCE/DOCKET NUMBER: 74940
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-616-5600
 TELEFAX: 312-616-5700
 INFORMATION FOR SEO ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 321 amino acids
 type: amino acid
 STRANDEDNESS: unknown

03-08-146-200-11

Query Match	39.1%;	Score 628.5;	DB 4;	Length 321;
Best Local Similarity	43.4%;	Pred. No. 4.9e-48;		
Matches 131;	Conservative 46;	Mismatches 124;	Indels 1;	Gaps 1;

[illegible]

RESULT 12
 US-08-467-948A-2
 Sequence 2, Application US/08467948A
 Patent No. 5998164
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 TITLE OF INVENTION: Coupled Receptor GPR2
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: STENE, KESSLER, GOLDSTEIN & FOX P. L. L. C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEEFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 2

```

; SEQUENCE CHARACTERISTICS:
;     LENGTH: 296 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;
US-08-467-948A-2

```

Query Match	38.7%;	Score 622.5;	DB 2;	Length 296;
Best Local Similarity	43.3%;	Pred. No. 1.5e-47;		
Matches 123;	Conservative 62;	Mismatches 98;	Indels 1;	Gaps 1;

QY	5	NDSTIOEIIIFGFDRLMEPLLEPLLVIVLISYTVIFPNLTIIIVSRDITLHPMPYELF	64
		: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	8	NOTWTEBELLIGLGRIGRIQMLFGLSLFVFLVLONGITLIGLISLDSRKHPTMYEFLS	67
QY	65	NLSLIDLCYTTCTIVPOMLVNLCISIRKVIYRGCVAOLFPLCATGATEYLLLVASFDMFY	124
		: : : : : : : : : : : : : : : : : : :	
Db	68	HLAVVNAIYACNTPQOMLVNLIHPAKRISFAGCGWTTDLFELSFANPECLLLVMSYDRYV	127
QY	125	AICRPRLHYAVIMHQRILCTOLAAASWVGEFNSVWLTSTLTLPDPCDDYVIDHFLCEVPAL	184
		: : : : : : : : : : : : : : : : : : : : : : : : : : :	
Db	128	AICRPRLKRFITMKVKCITLIGITSWTGSSLAMVHSLILRLPFCGREGRLNHPFCELSV	187
QY	185	LKLSCVETTANAEELFTVSELFHLPLTLILISYATFVRAVLRIQSAEGROKAFGTCSH	244
		: : : : : : : : : : : : : : : : : : : : : : : :	
Db	188	LRLCAADTLMNQVYIFEACMFILVGPCLIVYSYSHLIGLIRIOSEGRKRAFSTCSH	247
QY	245	LIVVSLFYSTVAIVYLDPSPSSSDGQKMSLFGGIIA-PLNLP	287
		: : : : : : : : : : : : : : : : : : : : : : : :	
Db	248	LCVVGLEFGSAIVMTMKSHNPEEQOKRFLLIQELSTPLPK	291

RESULT 13
US-08-467-947A-2
Sequence 2, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENIZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESSES:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600

RESULT 14
 US-08-118-270-61
 : Sequence 61, Application US/08118270
 : Patent No. 5508384
 :
 : GENERAL INFORMATION:
 : APPLICANT: Murphy, Randall B.
 : APPLICANT: Schuster, David I.
 : TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 : TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 : NUMBER OF SEQUENCES: 348
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEIMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 :
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/118,270
 : FILING DATE: 09-SEP-1993
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/943,236
 : FILING DATE: 10-SEP-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Townsend, Kevin G.
 : REGISTRATION NUMBER: 34,033
 : REFERENCE/DOCKET NUMBER: MURPHY-2A
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-628-5197
 : TELEFAX: 202-737-3528
 : TELEX: 248653
 :
 : INFORMATION FOR SEQ ID NO: 61:
 : SEQUENCE CHARACTERISTICS:

PCT-US93-08528-61
 RESULT 15
 : Sequence 61, Application PC/TUS9308528
 : GENERAL INFORMATION:
 : APPLICANT: New York University
 : TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 : TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 : NUMBER OF SEQUENCES: 348
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: BROWDY AND NEIMARK
 : STREET: 419 Seventh Street, N.W., Suite 300
 : CITY: Washington
 : STATE: D.C.
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US93/08528
 : FILING DATE: 09-SEP-1993
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: US 07/943,236
 : FILING DATE: 10-SEP-1992
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Townsend, Kevin G.
 : REGISTRATION NUMBER: 34,033
 : REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 202-628-5197
 : TELEFAX: 202-737-3528
 : TELEX: 248633
 : INFORMATION FOR SEQ ID NO: 61:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 284 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US93-08528-61

Query Match 37.1%; Score 596; DB 5; length 284;
Best Local Similarity 41.5%; Pred. No. 3,1e-45;
Matches 119; Conservative 52; Mismatches 112; Indels 4; Gaps 2;

```
QY 27 LTVVFLISYVTITFGNLTITLVSRDLKHPMYEFLLNLSLDDCYTCTVPQMLVNLG 86
      |::||| | : || || | : || || || || || || || || || || || || ||
Db 2 LFLFLIMYLAFTVGNLITITLIGGDSRLHTPMYFELSNLSFVDVCFSTTVPKVLNHI 61

QY 87 SIRKVISYRGCVAGLFEFLALGATEYILLVMSFDMFVAICRPLHYSVIMHORCLQDLAA 146
      : || : || : || : | : || || || : || || || || : | : || : |
Db 62 LGSQALISFSGCLTQLYFLAVFGNMNDFLAVMSYDRYVAICHPLHYTTI--RQLCVLLV 119

QY 147 ASWVTGFSNSVWLSTLTQLPLCDPYVIDHFICEVPALRLKSCVETTANEAELFLVSELF 206
      ||| | : : : | : || : || || | : || | : | | :
Db 120 GSWVYAMNCLHLILIMARKSPCAD--LPHFCDGTPLKLTSCSDTHLNLMLITBGA 177

QY 207 HLLPILLISYAFIVRAVLRIOGAEGRKAFGTGSHLIIVSLFYSTAVSVYLQPPSPS 266
      : | || || | || || : | : || || : || || : || || : || || |
Db 178 MVTPEVCILISYIHTCAVLRVSSPRGSKSFSTGSHIAVVCIFYGTVIAYVFNPSSSH 237

QY 267 SKDQKMWSLFYGLIAPMLNPLIYTLRNKEVKEGKRLVARVFLIKK 313
      : || : || : || : || || || || || || || || || || || || || ||
Db 238 LAGRDMAAAVAVTAVTPMNPFTYSLRNSDKAALRKVLAMRPPSKQ 284
```

Search completed: August 25, 2002, 20:07:59
Job time: 4222 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 25, 2002, 19:02:17 ; Search time 47.87 Seconds

(without alignments)
628.284 Million cell updates/sec

Title: US-09-800-321A-4

Perfect score: 1607

Sequence: 1 MMWVDSIIQEFILGFSDR.....NKEVGEKRLVAVFLIKK 313

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.71.*

1: p1r1.*

2: p1r2.*

3: p1r3.*

4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	902	56.1	312	2	A46247	olfactory receptor
2	851	53.0	316	2	A57069	olfactory receptor
3	747	46.5	315	2	JC5836	olfactory receptor
4	728	45.3	305	2	S29711	olfactory factor O
5	701	43.6	309	1	S51356	olfactory receptor
6	697	43.4	304	2	S29709	olfactory receptor
7	680	42.3	314	2	S29707	olfactory receptor
8	674.5	42.0	313	2	S20571	olfactory receptor
9	669	41.6	313	2	B23701	olfactory receptor
10	668.5	41.6	318	2	JC5202	olfactory receptor
11	661	41.1	315	2	JC4658	chemoreceptor TR64
12	660	41.1	319	2	JC5624	olfactory receptor
13	659	41.0	327	2	F23701	olfactory receptor
14	656	40.8	314	2	H23701	olfactory receptor
15	655	40.8	314	2	S20572	olfactory receptor
16	648.5	40.4	320	2	S20573	olfactory receptor
17	648	40.3	310	2	E23701	olfactory receptor
18	647	40.3	314	2	A37286	olfactory receptor
19	645	40.1	333	2	A23701	olfactory receptor
20	640	39.8	315	2	JC5201	chemoreceptor TR56
21	640	39.8	317	2	D23701	olfactory receptor
22	630	39.2	312	2	G23701	olfactory receptor
23	628	39.1	311	2	JC5200	chemoreceptor TR33
24	627.5	39.0	312	2	S29708	olfactory receptor
25	626.5	38.8	312	2	A48413	probable olfactory
26	623	38.8	312	2	I23701	olfactory receptor
27	611.5	38.1	312	2	S29710	olfactory receptor
28	602	37.5	311	2	G23701	olfactory receptor
29	570	35.5	312	2	A46750	olfactory receptor

30	527	32.8	264	2	PC4369	olfactory receptor
31	520	32.4	222	2	D40745	odorant receptor (
32	513	31.9	232	2	S29001	G protein-coupled
33	477	29.7	234	2	S29000	G protein-coupled
34	462	28.7	157	2	S58035	probable olfactory
35	455	28.3	216	2	I38480	olfactory receptor
36	450	28.0	222	2	B40745	odorant receptor (
37	448	27.9	216	2	I38470	olfactory receptor
38	444	27.6	216	2	I38474	olfactory receptor
39	444	27.6	234	2	S28998	G protein-coupled
40	441	27.4	234	2	S28999	G protein-coupled
41	440	27.4	216	2	I38481	olfactory receptor
42	437.5	27.2	225	2	I38478	olfactory receptor
43	434	27.0	216	2	I38479	olfactory receptor
44	434	27.0	216	2	I38476	olfactory receptor
45	423	26.3	216	2	I38477	olfactory receptor

ALIGNMENTS

RESULT 1
A46247
olfactory receptor OR3 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C:Accession: A46247
R:Nef, P.; Hermans-Borgmeyer, I.; Artieres-Pin, H.; Beasley, L.; Dionne, V.E.; Heinem
Proc. Natl. Acad. Sci. U.S.A. 89, 8948-8952, 1992
A:Title: Spatial pattern of receptor expression in the olfactory epithelium.
A:Reference number: A46247; MIMD:93028384
A:Accession: A46247
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-312 <NEF>
A:Cross-references: GB:M84005; NID:9200153; PIDN:AAA39862.1; PID:9200154
A>Note: sequence extracted from NCBI backbone (NCBIP:115362)
C:Superfamily: olfactory receptor OR14

Query Match 56.1%; Score 902; DB 2; Length 312;
Best Local Similarity 58.8%; Pred. No. 1.3e-72;
Matches 174; Conservative 46; Mismatches 76; Indels 0; Gaps 0;

QY 12 FILGSDRPMLEPPLVFLISTVTIFGNLTILVSRDLTKHTPMYFFLTNLSIDL 71
DB 12 FILMGSDPHLEIFFAVILASYLTLVGNLTILSRDLARLHTPMYFFLTNLSIDL 71
QY 72 CYTCTVPMILVNCISIRKVISYRCVADLFFILAGATEYLLAVMSFDWPAICRPLH 131
DB 72 APTTSSVPMKMLNGPRKTTISYGCVQTLVFLMAGATECILLVMAFDRVAVACRPLH 131
QY 132 YSVIHQRILQLAAASVWTFGSNSVWLTSTLTLQLPLCDPVYIDHFLCEVPALTKSCVE 191
DB 132 YMTVNPRLCGLAIAISWLGSGNSVISTFTLQLPFGCHGRKVDLNVMAFDRVAVACRPLH 191
QY 192 TTANAEFLVSEFLPLILISYAFYRAVLRIGASBGRQAAGTCSHLIVSLF 251
DB 192 TSLNVAVINGVCTFTTVPVSVILVSYCFIAOVAKIRISVEBRRRAFTCVSHLVVFLF 251
QY 252 YSTAVSVLPPSPSSKDGKMSVLFYGLIAPMLPLTYTLTKNKVKGKGFVLVAR 307
DB 252 YGSATVGLLPPKSSNOSQGRFISLFSVAVTPMPLTYTLTKNKVKGKALGRLK 307

RESULT 2
A57069
olfactory receptor FAT11 - human
C:Species: Homo sapiens (man)
C>Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 26-Aug-1999
C:Accession: A57069
R:Fan, W.; Liu, Y.C.; Parimoo, S.; Weissman, S.M.
Genomics 27, 119-123, 1995

A>Title: Olfactory receptor-like genes are located in the human major histocompatibility
A:Reference number: A57069; MUID:95394447
A:Accession: A57069
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-316 <FAN>
A:Cross-references: GB:I35475; NID:g1041044; PIDN:AAB3567.1; PID:g601919
C:Genetics:
A:Gene: GDB:FAT11; OLF2
A:Cross-references: GDB:I323249; OMIM:600578
A:Map position: 6p21.3-6p21.3
C:Superfamily: olfactory receptor OR14

Query Match	53.0%	Score 851	DB 2	Length 316	
Best Local Similarity	53.8%	Pred. No. 4.5e-68			
Matches 163	Conservative 52	Mismatches 86	Indels 0	Gaps 0	
QY	5	NDSIIIEFLLGFSDRPWLEFPRLVLFVLSYVTTEFGNTLLIRSLRDLTKLTPMYFELT	64		
Db	3	NQSSRPGFLLGFSHPHGRPLFPDVITSYLLTLGNLTLILSALDTRKLSHPMYFELS	62		
QY	65	NLSLIDLCYTTCTVPQMLVNLCSIRKVISYRGVAQLFETALGATEYLLAVNSFDFEV	124		
Db	63	NLSFIDLCTTSCVPMLANLWGPKKTISFLDCSQVQIFETLSIGTTECIKRMVAFDRYV	122		
QY	125	ALCRPLHSVINHQALCQLAASAVTGSNSVMSTLTLQRLCDPVYIDHFLCEVRL	184		
Db	123	ACQPLHATITTHPRICWOLASVAVIGLVGVSQVTPSTLHPFCPPDRQVDFVEVPRL	182		
QY	185	LKLSCEVTANAEELFLVSELPHLIRPLTLLISYAFIYAVLRIGSAEGRKAFGTCGH	244		
Db	183	TKLSEEDSYNRIQAVASVFLVYPLRLSLIYSGLTAITAVYLRINSATAMKRAFGTCSSH	242		
QY	245	LIVLSLFYSTAVSYLQRPSPSSKQDGKWSLFYGIAPMLNPDLIYTLNKEVKEGFKRL	304		
Db	243	LTVVTLFVSSYAVYLOPKNPYAQGRKPFGLFYAVGFPSLNPVYLTTLNKEIKRRLRL	302		
QY	305	VAR 307			
Db	303	LGR 305			

RESULT 3
JC5836
olfactory receptor-like protein 2 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 05-Mar-1998 #sequence_revision 13-Mar-1998 #text_change 24-Nov-1999
C:Accession: Jc5836
R:Blache, P.; Gros, L.; Salazar, G.; Bataille, D.
Biochem. Biophys. Res. Commun. 242, 669-672, 1998
A:Title: Cloning and tissue distribution of a new rat olfactory receptor-like
A:Reference number: Jc5836; M0ID:98125351
A:Accession: Jc5836
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-315 <BLA>
A:Cross-references: GB:AF029357; NID:g2570934; PID:g2570935
C:Comment: This protein is implicated in white cell maturation and migration.
C:Superfamily: olfactory receptor OR14
F:28-53/Domain: transmembrane #status predicted <TM1>
F:64-86/Domain: transmembrane #status predicted <TM2>
F:95-123/Domain: transmembrane #status predicted <TM3>
F:147-165/Domain: transmembrane #status predicted <TM4>
F:203-222/Domain: transmembrane #status predicted <TM5>
F:241-264/Domain: transmembrane #status predicted <TM6>
F:277-293/Domain: transmembrane #status predicted <TM7>

Query Match	46.58;	Score 747;	DB 2;	Length 315;
Best Local Similarity	46.28;	Pred. NO. 7.8e-59;		
Matches 139;	Conservative 71;	Mismatches 91;	Indels 0;	Gaps 0;

```

OY 5 NDSIQEQLLGGESRPLMEPLLVFLVFLISTVYIFGVLITILVSRDLTKLHTEPMFFL 64
   | : | | | | | | | | | : | : | : | | | | | : | : | | | | | | | |
Db 8 NCSVSFEILLGSSSESOIRNALFFELFLLMYTLLNGLIVALITYLDSRLHTMYEFLS 67
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 65 NLSLLDLCYTCYVQPMVLNCLSRKVISYRGCAOLEFIFLALGATEYLLAVNSFDMV 124
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 68 ILSIVDMSYVTYTTVQMLVNNVCPKRTISMGACVAAQMFIFVLGIAECVLTAIMAYDRI 127
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 125 AICRPLRHSVIMHQRLCIQLAAASWYGFSSNSWMLSTLTDLPLCDPYVIDHFLCEVPAL 184
   | | | | | | | | | : | : | : | : | | | | | | | | | | | | | | |
Db 128 AICFPLRHSVIMSRICVAKMYTICSSISVTGALITYVTMRLPCGPKKINHFCEVPAV 187
   | | | | | | | | | : | : | : | : | | | | | | | | | | | | | | |
OY 185 IKLQSVETTANDELFLVSELPHILPLILLISYAFIVRAVLRIQSAEGROKAGTGGSH 244
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 188 IKLACADTSFNDRLDELLGFVLLVPLSLIASTACIFVSLIRIRSSGGRKLSFTCASH 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 245 IIVSLFYSTAVSYVYLQPPSPSKDQGRMVSLEFGIILPMNLPIYTLRKNVEGEGRKL 304
   : | | : | | : | : | | | : | : | | | | : | : | | | | | | | | :
Db 248 ITVTYTMFGPAMVMYIMRGGSWYDPERDCKLLAFNVVSAFLNPITLYSLRNNDVGAKMKV 307
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
OY 305 V 305
   :
Db 308 L 308

RESULT 4
S29711
olfactory factor OR37 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 04-Sep-1998
C:Accession: S29711
R:Ramung, K., Krieger, J., Strotmann, J., Boehhoff, I., Kubick, S., Baumstark, C., Br
Nature 361, 353-356, 1993
A:Title: Cloning and expression of odorant receptors.
A:Reference number: S29707; MUID:93149273
A:Accession: S29711
A:Molecule type: mRNA
A:Residues: 1-305 <RAM>
C:Superfamily: olfactory receptor OR14

```

[illegible]

RESULT 5
S51356
olfactory receptor - rat

Db 245 LSVSLVFGVTIPIYLCPSSNNSTYKETFVMSLMTYIVLPMLNPIFYLSLRNDIK 298

RESULT 8

S20571

olfactory receptor - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 22-Nov-1993 #sequence-revision 01-Dec-1995 #text-change 26-Aug-1999

C:Accession: S20571

R:Parmentlier, M.; Libert, F.; Schumans, S.; Schifflmann, S.; Lefort, A.; Eggerickx, D.; Nature 355, 453-455, 1992

A:Title: Expression of members of the putative olfactory receptor gene family in mammals

A:Reference number: S20571; MUID:92131132

A:Accession: S20571

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1513 <PAR>

A:Cross-references: EMBL:X64966; NID:9890; PTDN:CAA46129.1; PID:9891

A:Superfamily: olfactory receptor OR14

A:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	42.0%;	Score 674.5;	DB 2;	Length 313;
Best Local Similarity	43.9%;	Pred. No. 2.1e-52;		
Matches 133;	Conservative 59;	Mismatches 110;	Indels 1;	Gaps 1;

OY		NDLSIOEPIIIIGGSDRWLEEFPLLVAFLLSYATTEICGNLTITLVSADPTKHTPEWFEFT	64
Db	5	NOTVASEFVLILGPIDPDQDLDLEYALFLAMAYTTTIGNLTLLIOLDSHHTPMKLIFS	64
OY		NLSLLDICVTTCVPOMLVNLCISIRRVYSRGCAOLFIFLAGATEYELLVAWSDFMV	124
Db	65	NLSRSDCLCFSSVMTPKLLQNMQOVSIPACGLTOMYFFELFGDLSESLVAAMAADRIV	124
OY		AICRPLHYSYMORLICLOAAASWTGFNSNWMLSTLLOPILDOPYIHDFICEPAL	184
Db	125	AICRPLPLTIMSKRLCFSLLVSWUTMTHAVHLHTLLMARLCFC-ANTIPHEDMSAL	183
OY		LKSCVETTYANEAELIVSFLPHLLPILLTLISYAFIVRAVLRIOSAEGRQKAFTGCSSH	244
Db	184	LKIASCPOTONEVLPIFMGLILVIIEPLLITTSYARIVSILIKVPSAIDICVFEGCSGH	243
OY		LIVLSLEYTAVSAYLOPPSPSSKDOKGWLSLEYGIIAAMLNPYLTLTKNKREVGSGFRLL	304
Db	244	LSVSLSELYGVIGILYCPSANNSTVAKETIMAMAYTVTFMLNPFIYSLRNKKDMKALKRRV	303
OY		VAR 307	
Db	304	ICR 306	

```

RESULT      9
B23701
Olfactory receptor F5 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 04-Sep-1998
C:Accession: B23701
R:Buck, L.; Axel, R.
Cell 65, 175-187, 1991
A:Title: A novel multigene family may encode odorant receptors: a molecular basis for od
A:Reference number: A23701; MUID:91191556
A:Accession: B23701
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-313 <BUC>
A:Cross-references: GB:M64377
C:Superfamily: olfactory receptor OR14
C:Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match	41.6%;	Score 669;	DB 2;	Length 313;
Best Local Similarity	42.8%;	Pred. No. 6.5e-52;		
Matches 134;	Conservative 53;	Mismatches 126;	Indels 0;	Gaps 0;

[illegible]

RESULT 10

JC5202

Chemoreceptor TB641 - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Feb-1997 #sequence_revision 2/-Feb-1997 #text-change 26-Aug-1999

C:Accession: JC5202; PC4304

R:Thomas, M.B.; Haines, S.L.; Akesson, R.A.

Gene 178, 1-5, 1996

F:Title: Chemoreceptors expressed in taste, olfactory and male reproductive tissues.

A:Reference number: JC5200; MUID:97080538

A:Accession: JC5202

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-318 <TH01>

A:Cross-references: GH:U0949; NID:g1256392; PIDN:AAC52911.1; PID:g1256393

A:Accession: PC4304

A:Status: preliminary

A:Molecule type: protein

A:Residues: 145-153; 245-253 <TH02>

A:Experimental source: taste bud

C:Comment: This protein is coupled to a GTP-binding protein-mediated signal transduction

C:Genetics:

A:Gene: tb641

A:Superfamily: olfactory receptor OR14

C:Keywords: olfaction; taste bud; transmembrane protein

F:30-53/Domain: transmembrane #status predicted <TM1>

F:63-84/Domain: transmembrane #status predicted <TM2>

F:106-125/Domain: transmembrane #status predicted <TM3>

F:145-159/Domain: transmembrane #status predicted <TM4>

F:202-224/Domain: transmembrane #status predicted <TM5>

F:243-265/Domain: transmembrane #status predicted <TM6>

F:276-296/Domain: transmembrane #status predicted <TM7>

Query Match	41.6%;	Score 668.5;	DB 2;	length 318;
Best Local Similarity	44.0%;	Pred. No. 7.3e-52;		
Matches 133;	Conservative 65;	Mismatches 101;	Indels 3;	Gaps 2;

QY 6 DSIIOEIIILGFSRPMLEPFLAVFLISVTVTFGNLLIIIVSRDPTKHT -PMYEFL 64
10 DTVVTDLFLGLAHPNMRFFLEFLVFLIIYITLQGNLILLLTYWADPKHARPMYLLG 69
Db 65 NLSLIDLCTTCTYPMQMLNLCSTRKIVISRGCAQOLFILAGATEYLLLAWSDFMEV 124
QY 70 VLSELDMLSSVIVPRILINFTPNPKAKIARGCGAOLYEFHFGISQCPFLTYTLMAADRYL 129
Db 125 AICRPILHYSVIMHORLCLQLAASWVGFNSVNLSTLTQLPLCDYVVIDHCELPVAL 184

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 25, 2002, 20:08:02 ; Search time 37.38 Seconds

(without alignments)
324.217 Million cell updates/sec

Title: US-09-800-321A-4

Perfect score: 1607

Sequence: 1 MNWVNSIIQEFILGFSDR.....NKEVKEGFKRLVAVFLIKK 313

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1593	99.1	313	1	O2B6_HUMAN
2	1295	80.6	357	1	O2B3_HUMAN
3	1130	70.3	313	1	O2B3_HUMAN
4	933	58.1	311	1	O2B3_HUMAN
5	904	56.3	312	1	O2B3_HUMAN
6	902	56.1	312	1	OLJ5_MOUSE
7	889	55.3	312	1	O2B2_HUMAN
8	885	55.1	316	1	O2B3_HUMAN
9	883	54.9	312	1	O2C1_HUMAN
10	871	54.2	320	1	O2M1_HUMAN
11	853	53.1	316	1	O2H1_HUMAN
12	804	50.0	317	1	OLF3_CANFA
13	779	48.5	317	1	O2F1_HUMAN
14	767	47.7	321	1	O5V1_HUMAN
15	766	47.7	317	1	O2E2_HUMAN
16	757	47.1	308	1	O2D2_HUMAN
17	711.5	44.3	309	1	O7AA_HUMAN
18	701	43.6	313	1	O1C1_HUMAN
19	697	43.4	315	1	O2S2_HUMAN
20	693.5	43.2	319	1	OAA4_HUMAN
21	691	43.0	309	1	OLP4_CANFA
22	688	42.8	314	1	O5F1_HUMAN
23	687	42.8	314	1	O5I1_HUMAN
24	687	42.8	320	1	O7C1_HUMAN
25	686	42.7	309	1	O7AH_HUMAN
26	683	42.5	312	1	OAC1_HUMAN
27	681	42.4	311	1	OLP2_CANFA
28	681	42.4	320	1	O7C2_HUMAN
29	680	42.3	311	1	OLP1_CANFA
30	680	42.3	312	1	OLP4_CHICK
31	679	42.3	313	1	O1G1_HUMAN
32	676	42.1	312	1	O1F1_HUMAN
33	675	42.0	313	1	OLF5_RAT

34	674.5	42.0	313	1	OLP2_CANFA	P30955 canis faml
35	669	41.6	311	1	O8B8_HUMAN	Q15620 homo sapien
36	668.5	41.6	310	1	O4D1_HUMAN	Q15615 homo sapien
37	668	41.6	317	1	OAA5_HUMAN	Q9H207 homo sapien
38	665	41.4	314	1	OAA3_HUMAN	P58181 homo sapien
39	663	41.3	318	1	OLP1_CHICK	P37067 gallus gall
40	662	41.2	310	1	O2A4_HUMAN	O95047 homo sapien
41	661	41.1	315	1	O3A1_HUMAN	P47881 homo sapien
42	660.5	41.1	307	1	OCB2_HUMAN	P58182 homo sapien
43	660	41.1	319	1	O7A5_HUMAN	Q15622 homo sapien
44	659	41.0	327	1	OLF7_RAT	P23270 rattus norv
45	658	40.9	312	1	OLF5_CHICK	P37071 gallus gall

ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	AA
O2B6_HUMAN				
AC	P58173; Q9H5B0;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Olfactory receptor 286 (Hs6M1-32) (Olfactory receptor 6-31) (OR6-31).			
GN	OR2B6.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Williams S.;			
RL	Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.			
CC	-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AL133267; CAC14158.1; .			
DR	InterPro; IPR000276; GPCR_Rhodopsn.			
DR	Pfam; PF00001; 7tm.1.1.			
DR	PRINTS; PR00237; GPCR_Rhodopsn.			
DR	PROSITE; PS00237; G-PROTEIN_RECP_FL1.1.			
DR	PROSITE; PS0262; G-PROTEIN_RECP_FL2.1.			
KW	G-protein coupled receptor; Transmembrane; Glycoprotein;			
KW	Multigene family; Olfaction.			
FT	DOMAIN 1 25			
FT	TRANSMEM 26 49			
FT	DOMAIN 50 57			
FT	TRANSMEM 58 79			
FT	DOMAIN 80 100			
FT	TRANSMEM 101 120			
FT	DOMAIN 121 138			
FT	TRANSMEM 140 158			
FT	DOMAIN 159 195			
FT	TRANSMEM 196 219			
FT	DOMAIN 220 236			
FT	TRANSMEM 237 259			
FT	DOMAIN 260 272			
FT	TRANSMEM 273 292			
FT	DOMAIN 293 313			
FT	DISULFID 97 189			
FT	CARBOHYD 5 5			
SQ	SEQUENCE 313 AA: 35414 MW: 71045954 IACF5501 CRC64;			

Query Match 99.1%; Score 1593; DB 1; Length 313;
 Best Local Similarity 99.7%; Pred. No. 3, 9e-112;
 Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNVNSIIIEFFILGSDRPMLEFPLVYVLLSYVTYTGNTITLIVSRIDTKLHPMY 60
 DB 1 MNVNSIIIEFFILGSDRPMLEFPLVYVLLSYVTYTGNTITLIVSRIDTKLHPMY 60

QY 61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAVOLFPLAGATEYLLAVMSF 120
 DB 61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAVOLFPLAGATEYLLAVMSF 120

QY 121 DMFVAICRPLHYSTVIMHORICLOLAASVWTGFSNSVWSTLTLOLPDCPYVIDHFCE 180
 DB 121 DMFVAICRPLHYSTVIMHORICLOLAASVWTGFSNSVWSTLTLOLPDCPYVIDHFCE 180

QY 181 VPALKLSCVETTANAEELFLVSEFLPLILPLILISYATVAVARIQSAEGRQKAFGT 240
 DB 181 VPALKLSCVETTANAEELFLVSEFLPLILPLILISYATVAVARIQSAEGRQKAFGT 240

QY 241 CGSHLIVSLFSTAVSVYIQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300
 DB 241 CGSHLIVSLFSTAVSVYIQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300

QY 301 FKRIVARVFLIKK 313
 DB 301 FKRIVARVFLIKK 313

RESULT 2
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 AC Q9GZK3; Q9GZL2; Q9Y299;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 2B2 (Olfactory receptor 6-1) (OR6-1) (Hs6M1-10).
 GN OR2B2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT ARG-234.
 RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,
 RA Volz A., Younger R., Beck S.;
 RT "Polymorphic olfactory receptor genes and HLA loci constitute extended
 haplotypes";
 RL (in) Kasaahara M. (eds.);
 RL Major histocompatibility complex-evolution, structure, and function,
 RL pp.110-130, Springer-Verlag, Tokyo (2000).
 RN [2]
 RP SEQUENCE OF 1-310 FROM N.A.
 RA Wild A.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@sib.ch).
 CC -----
 CC EMBL: AJ302584; CAC20504.1; -
 CC EMBL: AJ302585; CAC20505.1; -
 CC EMBL: AJ302586; CAC20506.1; -
 CC EMBL: AJ302587; CAC20507.1; -
 CC EMBL: AJ302588; CAC20508.1; -

DR EMBL: AJ302589; CAC20509.1; -
 DR EMBL: AJ302590; CAC20510.1; -
 DR EMBL: AJ302591; CAC20511.1; -
 DR EMBL: AJ302592; CAC20512.1; -
 DR EMBL: AJ302593; CAC20513.1; -
 DR EMBL: 298744; CAB1427.1; -
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCRHOOPS.
 DR PROSITE: PS00237; G-PROTEIN RECP.F1.1; 1.
 DR PROSITE: PS0262; G-PROTEIN RECP.F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction; Polymorphism;
 FT DOMAIN 1 25
 FT TRANSMEM 26 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 120
 FT DOMAIN 121 139
 FT TRANSMEM 140 158
 FT DOMAIN 159 195
 FT TRANSMEM 196 219
 FT DOMAIN 220 236
 FT TRANSMEM 237 259
 FT DOMAIN 260 272
 FT TRANSMEM 273 292
 FT DOMAIN 293 357
 FT DISULFID 97 189
 FT CARBOHYD 5 5
 FT VARIANT 234 234
 FT
 FT
 SQ SEQUENCE 357 AA; 40412 MW; 53E2F82820EC440A CRC64;
 /FTID=VAR_010943.
 Query Match 80.6%; Score 1295; DB 1; Length 357;
 Best Local Similarity 81.3%; Pred. No. 7, 3e-90;
 Matches 252; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNVNSIIIEFFILGSDRPMLEFPLVYVLLSYVTYTGNTITLIVSRIDTKLHPMY 60
 DB 1 MNVNSIIIEFFILGSDRPMLEFPLVYVLLSYVTYTGNTITLIVSRIDTKLHPMY 60

QY 61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAVOLFPLAGATEYLLAVMSF 120
 DB 61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAVOLFPLAGATEYLLAVMSF 120

QY 121 DMFVAICRPLHYSTVIMHORICLOLAASVWTGFSNSVWSTLTLOLPDCPYVIDHFCE 180
 DB 121 DMFVAICRPLHYSTVIMHORICLOLAASVWTGFSNSVWSTLTLOLPDCPYVIDHFCE 180

QY 181 VPALKLSCVETTANAEELFLVSEFLPLILPLILISYATVAVARIQSAEGRQKAFGT 240
 DB 181 VPALKLSCVETTANAEELFLVSEFLPLILPLILISYATVAVARIQSAEGRQKAFGT 240

QY 241 CGSHLIVSLFSTAVSVYIQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300
 DB 241 CGSHLIVSLFSTAVSVYIQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300

QY 301 FKRIVARVFL 310
 DB 301 FKRIVARVFL 310

QY 301 FKRIVAKSL 310
 DB 301 FKRIVAKSL 310

RESULT 3
 O2B3_HUMAN STANDARD; PRT; 313 AA.
 AC Q76000;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 2B3 (Olfactory receptor 6-4) (OR6-4) (Hs6M1-1).
 GN OR2B3.


```

OS Homo sapiens (Human) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN RP SEQUENCE FROM N.A.
RA Evans K.;
RL submitted (SRP-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,
RA Volz A., Younger R., Beck S.;
RT "Polymorphic olfactory receptor genes and HLA loci constitute extended
RT haplotypes.";
RL (In) Kasahara M. (eds.);
RL Major histocompatibility complex-evolution, structure, and function,
RL pp.110-130, Springer-Verlag, Tokyo (2000).
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CC -----
DR EMBL: AL022737; CAA18782.1; -
DR EMBL: AJ302537; CAC20462.1; -
DR EMBL: AJ302538; CAC20463.1; -
DR EMBL: AJ302539; CAC20464.1; -
DR EMBL: AJ302540; CAC20465.1; -
DR EMBL: AJ302541; CAC20466.1; -
DR EMBL: AJ302542; CAC20467.1; -
DR EMBL: AJ302543; CAC20468.1; -
DR EMBL: AJ302544; CAC20469.1; -
DR EMBL: AJ302545; CAC20470.1; -
DR EMBL: AJ302546; CAC20471.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_REC_P1.1; 1.
DR PROSITE: PS50262; G_PROTEIN_REC_P2.1; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multi-gene family; Olfaction.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 26 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 140 158 4 (POTENTIAL).
FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 196 219 5 (POTENTIAL).
FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).
FT TRANSSEM 237 259 6 (POTENTIAL).
FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).
FT TRANSSEM 273 292 7 (POTENTIAL).
FT DOMAIN 293 313 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 5 5 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 313 AA; 35542 MM; 786BFBIE7B624440 CRC64;

Query Match 70.3%; Score 1130; DB 1; Length 313;
Best Local Similarity 70.3%; Pred. No. 1.3e-77;
Matches 220; Conservative 34; Mismatches 59; Indels 0; Gaps 0;

1 MNWVDSIIQEFIIIGFDSDPWLEPPLLVFLISTYVLIIFGVLITLIYSRLDTKIKHTPY 60
1 NMWEVSSEPKETELIIGFSDRWLMQLPFLVLLISVTYTIIFGVNSTMVCCKTKHTPY 60

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OY		61	FEFLNLSLDDLCYTTCYPOMLVNCSIRKVISYRGVCAOEFPLATGATEYLAAVSF	120
Db		61	FEFLNLSLDDLCYTTCYTPHMLVNIQCCKKITSTAGCYAHLIIFALCATCELLAAVSF	120
OY		121	DMEVAICRPHYSVIYMORCLQIAAASWVTGSFNVSVLSTFLTQLDPCDYVIDHFICE	180
Db		121	DRYAIVCPEPLHYVYIMNWFCILRMAAFSMILIGFSNVLOSSLTILMPCRGHQEVDHFCE	180
OY		181	VPAIIKISCADCTKPLEALEFFESVILLIPVLLISIGFIAQAALKRSAEGROKAKGT	240
OY		241	CGSHLIIVSYLFYSYAVSVYLOPPSPSSKDQGKMYSLEFGITAPLMNPILIYLRNKVEVG	300
Db		241	CGSHRIIVSYLFYGRARIYVLOPPSPSTSNDQGMKMSLEFGITSMINSILYLRNKDKEA	300
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Db		301	EKLMPRIEFCKK	313
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AC	076001; O9GZK5; O9GZL4; O9GZL5;			
DT	16-OCT-2001 (Rel. 40, Created)			
DF	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Olfactory receptor 2J3 (Olfactory receptor 6-6) (OR6-6) (Hs6M1-3).			
GN	OR2J3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RP	Submitted (SEP-1998) to the EMBL/Genbank/DDBJ databases.			
RL	[2]			
RA	SEQUENCE FROM N.A., AND VARIANTS A-113; Q-226; I-228 AND M-261.			
RA	Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,			
RT	Volz A., Younger R., Beck S.;			
RT	"Polymorphic olfactory receptor genes and HLA loci constitute extended			
RT	haplotypes.";			
RL	(in) Kashara M. (eds.);			
RL	Major histocompatibility complex-evolution, structure, and function,			
RL	pp.110-130, Springer-Verlag, Tokyo (2000).			
CC	-1- FUNCTION: PUTATIVE ODORANT RECEPTOR.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; AL022727; CAA18783.1;			
DR	EMBL; AJ302547; CAC20472.1;			
DR	EMBL; AJ302548; CAC20473.1;			
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DR	EMBL; AJ302550; CAC20475.1;			
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DR	EMBL; AJ302552; CAC21440.1;			
DR	EMBL; AJ302553; CAC21441.1;			
DR	EMBL; AJ302554; CAC21442.1;			
DR	EMBL; AJ302555; CAC21443.1;			
DR	EMBL; AJ302556; CAC21444.1;			
DR	EMBL; AJ302557; CAC20477.1;			
DR	EMBL; AJ302558; CAC20478.1;			

DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECIP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction; Polymorphism.
 FT DOMAIN 1 28
 FT TRANSMEM 29 52
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 FT TRANSMEM 61 82
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 FT DOMAIN 124 142
 FT TRANSMEM 143 161
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 FT VARIANT 226 226
 FT VARIANT 228 228
 FT VARIANT 261 261
 FT SEQUENCE 311 AA: 34950 MM: 84201145B9D5AA68 CRC64;
 Query Match 58.1%; Score 933; DB 1; Length 311;
 Best Local Similarity 59.9%; Pred. No. 6.3e-63;
 Matches 181; Conservative 43; Mismatches 78; Indels 0; Gaps 0;

QY 4 VNDSTIOEILGFSDRPWLEFPLVFLISTVTYVTFEGNLTIIIVSRDLTKHTPEYFL 63
 DB 7 VASSEGEYFLVGFNSWPLEVIVFVVLIFLMTLIGLFIITLSYDLSHTPEYFL 66
 QY 64 TNLSDLCYTTCTVPOKLVNLCSTRKIVSYNGCAQLFIALGATEYELLVAWSEDF 123
 DB 67 SNLSFELDYTTSSIPOLVNLNMGPEKTSYAGCMQLFVALGTGECVLLVWMSYDRY 126
 QY 124 VACRPLHYSVTHORLCIQLAAASWVTGFSNVLSTLQLPDDPYVIDHFLCEVPA 183
 DB 127 AAVCRPLHYSVTHORLCIQLAAASWVTGFSNVLSTLQLPDDPYVIDHFLCEVPA 186
 QY 184 LKLSCEVTANAEALFLVSELFHILPLTLISYAFIVRAVLRIQASAGROKAFGTGCS 243
 DB 187 LRLSCVDTHVNLFLMTSSIFVLPLTLISYGAIVRAVLRIQASAGROKAFGTGCS 246
 QY 244 HLIVVSLPSTAVSYVLPSPSSKDGKMSVLFGLIAPMLNPLTYLTRNKEVKEGFR 303
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 DB 307 LM 308

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 02J2_HUMAN STANDARD: PRT: 312 AA.
 AC 076002; Q9GZK2; Q9GZL3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 GN Olfactory receptor 2J2 (Olfactory receptor 6-8) (OR6-8) (Hs6ml-6).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Evans K.;
 RN Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
 RP Siegel A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,
 RA Ziegler A., Younger R., Beck S.;
 RT "Polymorphic olfactory receptor genes and HLA loci constitute extended
 haplotypes."
 RL (in) Kasahara M. (eds.);
 RL Major histocompatibility complex-evolution, structure, and function,
 RL pp.110-130. Springer-Verlag, Tokyo (2000).
 CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL: AL027272; CAI18784.1; -
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 DR EMBL: AJ302573; CAC20493.1; -
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 DR EMBL: AJ302579; CAC20499.1; -
 DR EMBL: AJ302580; CAC20500.1; -
 DR EMBL: AJ302581; CAC20501.1; -
 DR EMBL: AJ302582; CAC20502.1; -
 DR EMBL: AJ302583; CAC20503.1; -
 DR InterPro: IPR00276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PROSITE: PS00237; G_PROTEIN_RECIP_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECIP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction; Polymorphism.
 FT DOMAIN 1 26
 FT TRANSMEM 27 50
 FT DOMAIN 51 58
 FT TRANSMEM 59 80
 FT DOMAIN 81 101
 FT TRANSMEM 102 121
 FT DOMAIN 122 140
 FT TRANSMEM 141 159
 FT DOMAIN 160 196
 FT TRANSMEM 197 220
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 FT TRANSMEM 238 260
 FT DOMAIN 261 273
 FT TRANSMEM 274 293
 FT DISULFID 294 312
 FT CARBOHYD 98 190
 FT VARIANT 74 74
 FT VARIANT 111 111
 FT VARIANT 146 146
 FT VARIANT 218 218

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 A -> T (IN 6M1-6*03).
 /FTID-VAR_010946.
 A -> V (IN 6M1-6*02 AND 6M1-6*03).
 /FTID-VAR_010947.
 A -> T (IN 6M1-6*02 AND 6M1-6*03).
 /FTID-VAR_010948.

SQ SEQUENCE 312 AA; 35204 MW; FB7D20BB2379C43E CRC64;

Query Match 56.3%; Score 904; DB 1; Length 312;
Best Local Similarity 59.9%; Pred. No. 9.2e-61;
Matches 176; Conservative 43; Mismatches 75; Indels 0; Gaps 0;

QY 12 FILFGSDPRWLEFPLLVFLISYVTITFGNTLIIVSRDLTKLHPMPFELNLSLDL 71
DB 13 FILFGSDPRWLEFPLLVFLISYVTITFGNTLIIVSRDLTKLHPMPFELNLSLDL 72
QY 72 CYTTCVPMQMLVLCIRKIVSYRGCAVOLFIFLAGATEYLLAAVSPFMAICRPLH 131
DB 73 CHTTSSIPDLVNLKRGPEKTIISYAGCVDLYFVLAIGACVLLVMSYDRIYAVCRPLH 132
QY 132 YSIVMHQRCLQLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 191
DB 133 YVIMHPRCHLLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 192
QY 192 TTANAELEFVSEFLPLILPLILISYAFIVRAVLRIGSAGKQKAFGTGSHLIYVSLE 251
DB 193 TTANAELEFVSEFLPLILPLILISYAFIVRAVLRIGSAGKQKAFGTGSHLIYVSLE 252
QY 252 YSIVMHQRCLQLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 305
DB 253 YSIVMHQRCLQLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 306

RESULT 6
OL15_MOUSE STANDARD; PRT; 312 AA.
AC P23275;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Olfactory receptor 15 (OR3).
GN OLFR15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93028384; PubMed=1384038;
RA Neft P., Hermans-Borgmeyer I., Artieres-pin H., Beasley L.,
RA Dionne V.E., Heinemann S.F.;
RT "Spatial pattern of receptor expression in the olfactory epithelium.";
RT Proc. Natl. Acad. Sci. U.S.A. 89:8948-8952(1992).
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: OLFACTORY EPITHELIUM.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC -----
DR EMBL; M84005; AAA39862.1; -;
DR GCRDB; GCR_0494; -;
DR MGD; MGI:106182; Olfr15.
DR InterPro; IPR000276; GPCR_rhodpsn.
DR Pfam; PF00001; 7tm1.1;
DR PRINTS; PR00245; OLFACTORYR.
DR PROSITE; PS00237; G_PROTEIN_RECEP_FL_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_FL_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Olfaction; Multigene family.
FT DOMAIN 1 24 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 25 48 1 (POTENTIAL).

FT DOMAIN 49 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 79 2 (POTENTIAL).
FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 101 120 3 (POTENTIAL).
FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 160 4 (POTENTIAL).
FT DOMAIN 161 200 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 201 222 5 (POTENTIAL).
FT DOMAIN 223 236 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 237 261 6 (POTENTIAL).
FT DOMAIN 273 292 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 293 312 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 189 BY SIMILARITY.
FT CARBOHYD 6 6 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 312 AA; 34333 MW; 8D3877EBB5F1E132 CRC64;

Query Match 56.1%; Score 902; DB 1; Length 312;
Best Local Similarity 58.8%; Pred. No. 1.3e-60;
Matches 174; Conservative 46; Mismatches 76; Indels 0; Gaps 0;

QY 12 FILFGSDPRWLEFPLLVFLISYVTITFGNTLIIVSRDLTKLHPMPFELNLSLDL 71
DB 12 FILFGSDPRWLEFPLLVFLISYVTITFGNTLIIVSRDLTKLHPMPFELNLSLDL 71
QY 72 CYTTCVPMQMLVLCIRKIVSYRGCAVOLFIFLAGATEYLLAAVSPFMAICRPLH 131
DB 72 ARTTSSVPMQMLVLCIRKIVSYRGCAVOLFIFLAGATEYLLAAVSPFMAICRPLH 131
QY 132 YSIVMHQRCLQLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 191
DB 132 YSIVMHQRCLQLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 191
QY 192 TTANAELEFVSEFLPLILPLILISYAFIVRAVLRIGSAGKQKAFGTGSHLIYVSLE 251
DB 192 TTANAELEFVSEFLPLILPLILISYAFIVRAVLRIGSAGKQKAFGTGSHLIYVSLE 251
QY 252 YSIVMHQRCLQLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 307
DB 252 YSIVMHQRCLQLAAASWVTFGSNSVWLSLTLLQLPLCDPYVIDHFLCEVPALLKLSCE 307

RESULT 7
O2H2_HUMAN STANDARD; PRT; 312 AA.
ID O2H2_HUMAN
AC 095018;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 2H2 (Hs6M1-12).
GN O2H2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Younger R.;
RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL031983; CAA21455.1; -;

Query Match 55.1%; Score 885; DB 1; Length 316;
 Best Local Similarity 56.1%; Pred. No. 2.4e-59;
 Matches 170; Conservative 50; Mismatches 83; Indels 0; Gaps 0;

5 NSDIIOEFLIGSDRPMLEFPLLVFLISYTYIFGNLTIIIVSRIDTFLHPTMFEFL 64
 3 NOSTPGEFLIGSEHPGERTLEFVVVTSYLLTGLVNTLIIILSALDPKLSHSPMFEFLS 62
 65 NLSLDLCYTCVPMQMLVNLCSIRKIVSYRGCAOLFPLALGATEYLLAVMSFDMFV 124
 63 NLSFDLCCTTSQVPMQMLVNLGPKTISFLDSSVQIFILSGTTCILLTYMAEDPRIV 122
 125 AICRPLHYSVIMHQRCLQDLAASWTFGFSNYSWLTSLQDLPCDPYVIDHFLCEVPAL 184
 123 AVCPHLHYATIIHPRLCWQLASVAWVIGLVESVQTPSTLHLDFPCPDQGVDFVECPVAL 182
 185 LKISCVETANAEMLFLVSLFHLIPLTLLISYAFIVRAVLAIQSAEGKQKAFGTGSH 244
 183 IRLSCEDTSYNEIQVAVSVFLLVPLSLIVSGAITWAVLINSKGRKAFGTGSSH 242
 245 LTVSLFYSYTAASVYLOPPSPSSKDOGKMWLSFYGIAPMLNPLIYTLRKKEVKEGFKRL 304
 243 LTVVTLFYSYVIAVYLOPKRNPYAQERKGFGLTAYAGTSPSLNPLIYTLRKKEVTRAFRRL 302
 305 VAR 307
 303 LGR 305

RESULT 9
 02C1_HUMAN STANDARD; PRT; 312 AA.
 AC 095371;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 2C1 (OLFMT3).
 GN OR2C1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99063798; PubMed=9847080;
 RA Centola M., Chen X., Sood R., Deng Z., Aksemitjevich I., Blake T.,
 RA Ricks D., Chen X., Wood G., Zaks N., Richards N., Krizman D.,
 RA Mansfield E., Apostolou S., Liu J., Shafran N., Vedula A., Hanon M.,
 RA Cereek A., Kahan T., Gunculo D., Callen D.F., Richards R.T.,
 RA Moyzis R.K., Doggett N.A., Collins F.S., Liu P.P.,
 RA Fischel-Ghodsian N., Kastner D.L.;
 RT *Construction of an approximately 700 kb transcript map around the
 RT familial mediterranean fever locus on human chromosome 16p13.3.";
 RL Genome Res. 9:1-21(1998).
 CC - FUNCTION: PUTATIVE ODORANT RECEPTOR.
 CC - SUBCELLULAR LOCATION: Integral membrane protein.
 CC - SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF098664; AAC83557.1; -
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL_1; 1.

DR PROSITE: PS0262; G_PROTEIN_RECEPTOR_FL_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 25
 FT TRANSMEM 26 49
 FT DOMAIN 50 57
 FT TRANSMEM 58 79
 FT DOMAIN 80 100
 FT TRANSMEM 101 120
 FT DOMAIN 121 139
 FT TRANSMEM 140 158
 FT DOMAIN 159 196
 FT TRANSMEM 197 219
 FT DOMAIN 220 236
 FT TRANSMEM 237 259
 FT DOMAIN 260 272
 FT TRANSMEM 273 292
 FT DOMAIN 293 312
 FT DISULFID 97 189
 FT CARBOHYD 5 5
 SQ SEQUENCE 312 AA; 34506 MW; CCAD7D349BB8B9E7 CRC64;

Query Match 54.9%; Score 883; DB 1; Length 312;
 Best Local Similarity 55.7%; Pred. No. 3.4e-59;
 Matches 171; Conservative 51; Mismatches 85; Indels 0; Gaps 0;

1 MNVNDIIIOEFLIGSDRPMLEFPLLVFLISYTYIFGNLTIIIVSRIDTFLHPTMFEFL 60
 1 MDGVNDSILOGFVLMSTSDHPQLEMFIALFESYLLTGLNSTIIILSRLEARLHPTMFEFL 60
 61 PELTNLSLDLCYTCVPMQMLVNLCSIRKIVSYRGCAOLFPLALGATEYLLAVMSF 120
 61 FFLSNLSLDLCYTCVPMQMLVNLCSIRKIVSYRGCAOLFPLALGATEYLLAVMSF 120
 61 FFLSNLSLDLCYTCVPMQMLVNLCSIRKIVSYRGCAOLFPLALGATEYLLAVMSF 120
 121 DMFAICRPLHYSVIMHQRCLQDLAASWTFGFSNYSWLTSLQDLPCDPYVIDHFLCE 180
 121 DRYVAVCRPLHYSVIMHQRCLQDLAASWTFGFSNYSWLTSLQDLPCDPYVIDHFLCE 180
 121 DRYVAVCRPLHYSVIMHQRCLQDLAASWTFGFSNYSWLTSLQDLPCDPYVIDHFLCE 180
 181 VPALKLSCVETANAEMLFLVSLFHLIPLTLLISYAFIVRAVLAIQSAEGKQKAFGT 240
 181 VPMIKRLACGDTSLNQAVLVNGVCFPAVPLSTIVISYCLIAQVNLHSAEGKRAKAFNT 240
 241 CGSHLIVSLFYSYTAASVYLOPPSPSSKDOGKMWLSFYGIAPMLNPLIYTLRKKEVKEG 300
 241 CLSHLIVSLFYSYTAASVYLOPPSPSSKDOGKMWLSFYGIAPMLNPLIYTLRKKEVKEG 300
 301 FKRLVAR 307
 301 LRLILGR 307

RESULT 10
 02M1_HUMAN STANDARD; PRT; 320 AA.
 AC 093393; 09GZL0; 09GZL1;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Olfactory receptor 2M1 (Hs6M1-15).
 GN OR2M1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Smith S.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-81 AND ASN-296.
 RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,
 RA Volz A., Younger R., Beck S.;

RT "Polymorphic olfactory receptor genes and HLA loci constitute extended haplotypes." ;

RL (in) Kasahara M. (eds.);

RL Major histocompatibility complex-evolution, structure, and function, pp.110-130, Springer-Verlag, Tokyo (2000).

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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DR EMBL: AJ035402; CAB2853.1; -

DR EMBL: AJ302594; CAC20514.1; -

DR EMBL: AJ302595; CAC20515.1; -

DR EMBL: AJ302596; CAC20516.1; -

DR EMBL: AJ302597; CAC20517.1; -

DR EMBL: AJ302598; CAC20518.1; -

DR EMBL: AJ302599; CAC20519.1; -

DR EMBL: AJ302600; CAC20520.1; -

DR EMBL: AJ302601; CAC20521.1; -

DR EMBL: AJ302602; CAC20522.1; -

DR EMBL: AJ302603; CAC20523.1; -

DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; 7tm.1.1.

DR PRINTS: PR00237; GPCRHOPOPSN.

DR PROSITE: PS00237; G-PROTEIN_RECPT_FL1; 1.

DR PROSITE: PS50262; G-PROTEIN_RECPT_FL2; 1.

KM G-protein coupled receptor. Transmembrane; Glycoprotein; Multigene family; Olfaction; Polymorphism.

KM DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 26 49 1 (POTENTIAL).

FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 58 79 2 (POTENTIAL).

FT DOMAIN 80 100 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 101 120 3 (POTENTIAL).

FT DOMAIN 121 139 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 140 158 4 (POTENTIAL).

FT DOMAIN 159 195 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 196 219 5 (POTENTIAL).

FT DOMAIN 220 236 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 237 259 6 (POTENTIAL).

FT DOMAIN 260 272 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 273 292 7 (POTENTIAL).

FT DOMAIN 293 320 CYTOPLASMIC (POTENTIAL).

FT DISULFID 97 189 BY SIMILARITY.

FT CARBOHYD 5 5 N-LINKED (GLCNAC...) (POTENTIAL).

FT VARIANT 81 81 M -> V (IN 6M1-15*03).

FT VARIANT 81 81 /FTID-VAR_010953.

FT VARIANT 296 296 D -> N (IN 6M1-15*02).

FT VARIANT 296 296 /FTID-VAR_010954.

FT SEQUENCE 320 AA; 36101 MW; 7A8BCD3F443E1D0 CRC64;

QY Query Match 54.2%; Score 871; DB 1; Length 320;

QY Best Local Similarity 55.1%; Pred. No. 2.7e-58;

QY Matches 168; Conservative 51; Mismatches 86; Indels 0; Gaps 0;

DB 1 MNVNDIIIOEFLGSDRPMLEPFLVFLSYTIPGNTITIVSLDTRKLRPMY 60

DB 1 MDSQNTSSLHGFLGFSNFKMEMILSGVAIFYLITLGNATIIIASLDSQLRPMY 60

QY 61 FFLNLSLDLCYCTCTPQMLVNLCSIRKVISYRCVADLFELALGATEYLLAVMSF 120

DB 61 FFLNLSLDLCYCTCTPQMLVNLCSIRKVISYRCVADLFELALGATEYLLAVMSF 120

QY 121 DMVVALCRPLHYSVMHQRCLDOLAASVWTGSSNSVWLTSLQLPCLDPYVIDHFLCE 180

DB 121 DRETAICKPLHYEVNMPHCLKMIIMWISLANSVVLCTLTINLPTCGNNIIDHFLCE 180

QY 181 VPALLKLSCEVETPANEAEFLVSELFLPIPLTILISYAFVRAVLRIQSAEGROKAFGT 240

DB 181 LPAVLKACADDTTVEHSEVVALGIIVLPILILISYIAKAVLTKSAOSRKAMNT 240

QY 241 CGSHLVVMSFYSTAVSVYIQPSPPSSKDGKMSLFYGIIAPMLNPLIYTLRKEVKEG 300

DB 241 CGSHLVVMSFYSTAVSVYIQPSPPSSKDGKMSLFYGIIAPMLNPLIYTLRKEVKEG 300

QY 301 FKRLV 305

DB 301 LKKLM 305

RESULT 11

O2HL_HUMAN

ID O2HL_HUMAN STANDARD; PRT; 316 AA.

AC Q9GZK4; Q9GZK9; O43661; O43629;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Olfactory receptor 2H1 (Hs6M1-16) (Olfactory receptor 6-2) (OR6-2)

DE (OLFR42A-9004.14/9026.2).

GN OR2HL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A., AND VARIANT ASN-63.

RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B., Volz A., Younger R., Beck S.;

RT "Polymorphic olfactory receptor genes and HLA loci constitute extended haplotypes." ;

RL (in) Kasahara M. (eds.);

RL Major histocompatibility complex-evolution, structure, and function, pp.110-130, Springer-Verlag, Tokyo (2000).

RN [2]

RP SEQUENCE FROM N.A.

RA Whitaker H.;

RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE OF 58-251 FROM N.A.

RA Galliano H.;

RT "Olfactory receptor gene cluster in man and mouse major histocompatibility complex." ;

RL Immunogenetics 0:0-0(1998).

RN [4]

RP SEQUENCE OF 58-251 FROM N.A.

RA Amadou C., Avoustin P., Ribouchon M.T., Bouissou C., Tazi Ahnini R., Ayer C., Portarotti P.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL: AJ302604; CAC20524.1; -

DR EMBL: AJ302605; CAC20525.1; -

DR EMBL: AJ302606; CAC20526.1; -

DR EMBL: AJ302607; CAC20527.1; -

DR EMBL: AJ302608; CAC20528.1; -

DR EMBL: AJ302609; CAC20529.1; -

DR EMBL: AJ302610; CAC20530.1; -

DR EMBL: AJ302611; CAC20531.1; -

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RP SEQUENCE FROM N.A.
RA Issel-Tarver L., Rine J.;
RL Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Bauer C., Williams D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CC
DR EMBL: U56421; AAB01215.1; -
DR EMBL: AC004653; AAC64376.1; -
DR GCRDB: GCR_1924; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 24
FT TRANSMEM 25 48
FT TRANSMEM 49 57
FT TRANSMEM 58 79
FT DOMAIN 80 100
FT TRANSMEM 101 120
FT TRANSMEM 121 139
FT TRANSMEM 140 160
FT TRANSMEM 161 200
FT TRANSMEM 201 222
FT DOMAIN 223 236
FT TRANSMEM 237 261
FT TRANSMEM 262 272
FT TRANSMEM 273 292
FT TRANSMEM 293 317
FT DISULFID 97 189
FT CARBOHYD 5 5
FT CONFLICT 211 211
SQ SEQUENCE 317 AA; 35350 MW; A72ADE1AEB680CE CRC64;
F -> L (IN REF. 1). (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
Query Match 48.5%; Score 779; DB 1; Length 317;
Best Local Similarity 49.8%; Pred. No. 1.9e-51; Indels 0; Gaps 0;
Matches 150; Conservative 58; Mismatches 93;
QY 5 NDSIIQEFILGFSRDMWLEFPLLVVLLSYTYIFGNLTIIIVSRDTRLHTPMYFFLT 64
DB 5 NQWVSEFILLGLSSDMDFRVSLFVLFVMTVTVGNCLIVLIRDSLHTPMYFFLT 64
QY 65 NLSLDDCYTTCVTPQMLVNLCSIRKIVSYRGCAQLFTFLAIGATEYLLLAWSQDWEV 124
DB 65 NLSLVDSYATSVVPCLLAFLAEHKAIPFOCAAOLEFSLAIGIEFVLLAVMAYDRYV 124
QY 125 AICRPLHYSIMHORLCLOLAASWVYGFNSWLSLTITOLPDCDXYVDHFLCEPAL 184
DB 125 AVCDALYSAIMHGGLCARLAITSWSGFTSSPVQTAITPQLPCKRKKFDHISCELLAV 184
QY 185 LKISCVEETNEAEELPFLPLTLILISAFIVRAVLRIQSEGRKAFGTCGSH 244
DB 185 VRLACVDTSSNEVTIMSSIVLMTPTCVLLSLTIQIISITLKIQSEGRKKAFFHCASH 244

QY 245 LTVVSLFYSTAVSYLQPPSPSSKDQKMWSLFYGIAPMLNPLIYLRNKEVGEGRKL 304
DB 245 LTVVSLFYSTAVSYLQPPSPSSKDQKMWSLFYGIAPMLNPLIYLRNKEVGEGRKL 304
QY 305 V 305
DB 305 L 305
RESULT 14
ID 05VL_HUMAN STANDARD; PRT; 321 AA.
AC 09UGF6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Olfactory receptor 5VL (Hs6M1-21).
GN OR5V1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN
RN SEQUENCE FROM N.A.
RP Tracey A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC
CC -1- FUNCTION: PUTATIVE ODORANT RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: AL096770; CAB65797.1; -
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCRHOOPS.
DR PROSITE: PS00237; G-PROTEIN_RECEPT_F1_1; 1.
DR PROSITE: PS0262; G-PROTEIN_RECEPT_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 25
FT TRANSMEM 26 49
FT TRANSMEM 50 57
FT TRANSMEM 58 79
FT TRANSMEM 80 100
FT TRANSMEM 101 120
FT TRANSMEM 121 139
FT TRANSMEM 140 158
FT TRANSMEM 159 195
FT TRANSMEM 196 219
FT DOMAIN 220 236
FT TRANSMEM 237 259
FT TRANSMEM 260 272
FT TRANSMEM 273 292
FT TRANSMEM 293 321
FT DISULFID 97 189
FT CARBOHYD 5 5
SQ SEQUENCE 321 AA; 36056 MW; AAC426DFCE58E375 CRC64;
N-LINKED (GLCNAC. .) (POTENTIAL).
Query Match 47.7%; Score 767; DB 1; Length 321;
Best Local Similarity 49.3%; Pred. No. 1.5e-50; Indels 0; Gaps 0;
Matches 148; Conservative 53; Mismatches 99;
QY 5 NDSIIQEFILGFSRDMWLEFPLLVVLLSYTYIFGNLTIIIVSRDTRLHTPMYFFLT 64
DB 5 NQWVSEFILLGLSSDMDFRVSLFVLFVMTVTVGNCLIVLIRDSLHTPMYFFLT 64

[illegible]

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SQ      SEQUENCE      317 AA;  35293 MM;  031EA92D9A60720C CRC64;
Query Match      47.7%;  Score 766;  DB 1;  Length 317;
Best Local Similarity 48.5%;  Pred. No. 1.8e-50;
Matches 147;  Conservative 63;  Mismatches 93;  Indels 0;  Gaps 0;

QY      5  NDSIIQEFILIGFSRPMLEPPLLVFLISTYVNIIFGNLTIIIVSRIDPTKIHFTPMYFELT 64
Db      5  NQIWRREFILIGLSDMCTQIISLFSFLVITLMTVLGNCILIVLIRLDSRLHPTMYFELT 64
QY      65  NLSLDLCTTCTVPMQLVNLCSIRKVISYRGVAQAQIFPLALGATEYLLAVNSFDMFV 124
Db      65  NLSIVDVSYATSVPQLLAHFLAEHKAIPFGSCAAQLFFESLALGIEFVLLAVMAYDRHV 124
QY      125  AICRPLHYSYIMHORLCLQLAASWYTFGSNSWMLSTITDLPICDPYVIDHFLCEVPAL 184
Db      125  AVSDRLRISAIMHGGLCARLAITSWVSGSINSLVOTAITFDLPMTCKNFIDHISCELLAV 184
QY      185  LKLSCEVTANEADELFLVSELFLHPIPLILILISYAFIVRAVLRIQASAGROKAFGTCGSH 244
Db      185  VRLACVDSNSNEAAMWSSIVLLMPFCLVLLSYRIIISTLIKIQSRGRKKAFHTCASH 244
QY      245  LIIVSLFYSTAVSYVLIQPPSPSSKDQGMVSLFQIIAPMLNPLIYTLRNKEVKEGEFKRL 304
Db      245  LTVVALCYGTITFTYIQPHSGPSVLOEKRLISVFAYVAPLNPVIYSLRNKEVKGAMHKL 304
QY      305  VAR 307
Db      305  LEK 307

Search completed: August 25, 2002, 20:17:50
Job time: 588 sec

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Search completed: August 25, 2002, 20:17:50
Job time: 588 sec
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N-LINKED (GLCNAC. . .) (POTENTIAL)

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 25, 2002, 20:07:32 ; Search time 87.97 Seconds

(without alignments)
615.521 Million cell updates/sec

Title: US-09-800-321A-4

Perfect score: 1607

Sequence: 1 MNWVNDSTIOEFGFILLGFSDR.....NKEVKEGPKRLVARYFLINK 313

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 562222 segs, 17294929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1259	78.3	313	11	063394
2	1098	68.3	216	4	043883
3	917	57.1	312	4	09GZK6
4	915	56.9	312	4	09GZK1
5	908	56.5	310	11	09WV14
6	892	55.5	302	11	09GZK1
7	881	54.8	312	11	09WV11
8	872	54.3	312	11	09R022
9	867	54.0	317	11	092305
10	865	53.8	312	11	09WV13
11	857.5	53.4	314	4	09S499
12	802	49.9	318	11	092022
13	793	49.3	314	11	09EPG5
14	783	48.7	314	11	09EPG6
15	778	48.4	307	11	09EPG0
16	774	48.2	317	11	0923R1

17	771	48.0	312	11	09QZ18	09QZ18 mus musculu
18	769	47.9	318	11	09QZ21	09QZ21 mus musculu
19	768	47.8	307	11	09EP9	09EP9 mus musculu
20	767	47.7	307	11	09EP67	09EP67 mus musculu
21	766	47.7	307	11	09EPV1	09EPV1 mus musculu
22	764	47.5	216	4	096R13	096R13 homo sapien
23	753	46.9	310	11	09EP55	09EP55 mus musculu
24	752	46.8	312	13	090808	090808 gallus gall
25	752	46.8	318	11	09QZ20	09QZ20 mus musculu
26	752	46.8	319	11	09QZ22	09QZ22 mus musculu
27	747	46.5	315	11	035434	035434 rattus norv
28	738	45.9	319	11	09QZ19	09QZ19 mus musculu
29	734.5	45.7	315	11	09JKA6	09JKA6 mus musculu
30	728	45.3	305	11	09QW38	09QW38 rattus sp.
31	719	44.7	237	11	09R0G5	09R0G5 marmota mar
32	718	44.7	312	11	09ECB1	09ECB1 mus musculu
33	714	44.4	310	11	09ECB0	09ECB0 mus musculu
34	712	44.3	332	13	090806	090806 gallus gall
35	711	44.2	309	11	09JHB2	09JHB2 mus musculu
36	707	44.0	309	11	09ECB8	09ECB8 mus musculu
37	703	43.7	308	13	09EX09	09EX09 ambystoma t
38	702	43.7	308	11	09EC98	09EC98 mus musculu
39	701	43.6	309	11	063395	063395 rattus norv
40	699	43.5	313	6	09TU86	09TU86 gorilla gor
41	697	43.4	304	11	09QW36	09QW36 rattus sp.
42	695.5	43.3	310	11	09ECB7	09ECB7 mus musculu
43	695	43.2	310	11	09JHW3	09JHW3 mus musculu
44	695	43.2	313	11	09ECB3	09ECB3 mus musculu
45	694	43.2	309	11	09ECG1	09ECG1 mus musculu

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	313 AA.
ID	063394			
AC	063394;			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	OL1 RECEPTOR.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-SPRACUE-DAWLEY;			
RX	MEDLINE=96172460; PubMed=8589991;			
RA	Dutrel G., Arrang J.M., Diaz J., Wisniewsky C., Schwartz K.,			
RA	Schwartz J.C.;			
RT	"Cloning of OL1, a putative olfactory receptor and its expression in			
RT	the developing rat heart."			
RL	Recept. Channels 3:33-40(1995).			
EMBL	L34074; AAC31675.1; -.			
DR	InterPro: IPR002106; GPCR_Rhodopsin.			
DR	InterPro: IPR002106; GPCR_Rhodopsin.			
DR	Pfam: PF00001; 7tm.1; 1.			
DR	PROSITE: PS00339; AA_TRNA_LIGASE_II.2; UNKNOWN_1.			
DR	PROSITE: PS00237; G_PROTEIN_RECEPTOR_1; UNKNOWN_1.			
DR	PROSITE: PS0262; G_PROTEIN_RECEPTOR_1.			
KW	RECEPTOR.			
SQ	SEQUENCE 313 AA; 35434 MW; 6BDADD83AAC34D37 CRC64;			

Query Match	78.3%	Score 1259;	DB 11;	Length 313;
Best Local Similarity	78.0%;	Pred. No. 2e-108;		
Matches 244;	Conservative 29;	Mismatches 40;	Indels 0;	Gaps 0;
Oy	1 MNWVNDSTIOEFGFILLGFSDRPWLEPLFVYFLVSYILITFGNMIIIVSRIDSLRHPMY 60			
Db	1 MSVANEISREFFILGFSDRPWLEPLFVYFLVSYILITFGNMIIIVSRIDSLRHPMY 60			

QY 61 FFLTNLSLDLCYTTCTVPQMLVNLCSIRKVISYRGCAVLFLALGATEYLLAVMSF 120
 DB 61 FFLTNLSLDLCYTTCTVPQMLNLCSTRKVISYGCVAQLFLFLSGSTECFLGWSL 120
 QY 121 DMFVATCRPLHYVIMQRLCLQLAASWYTGFSNSWMLSTLTQLPLCDPYVDHFLCE 180
 DB 121 DRLAICRPLHYVIMQRLCLQLAASWYTGFSNSWMLSTLTQLPLCDPYVDHFLCE 180
 QY 181 VPALLKLSCEVTANEAELELVSELFLHILPLTLILISYAFIVRAVLRIQSAEGKRAFGT 240
 DB 181 VPALLKLSCEVTANEAELELVSELFLHILPLTLILISYAFIVRAVLRIQSAEGKRAFGT 240
 QY 241 CGSHLIVVLFYFGATVIMYLOPPSPSSKDGKMWLSFYGIAPMLNPLIYLRNKEVKEG 300
 DB 241 CGSHLIVVLFYFGATVIMYLOPPSPSSKDGKMWLSFYGIAPMLNPLIYLRNKEVKEG 300
 QY 301 FKRLVARVFLIKK 313
 DB 301 FKRLMKRIILIGK 313

RESULT 2
 ID 043883 PRELIMINARY; PRT; 216 AA.
 AC 043883;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE OLFACTORY RECEPTOR (FRAGMENT).
 GN OR5-40.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98160182; PubMed=9500546;
 RA Rouquier S., Taviaux S., Trask B.J., Brand-Arpon V., van den Engh G.,
 RA Demallie J., Giorl D.;
 RT "Distribution of olfactory receptor genes in the human genome."
 RL Nat. Genet. 18:243-250(1998).
 DR EMBL: U86270; AAC39628.1;
 DR InterPro: IPR002106; AA_CRNA_ligase_II.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF0001; 7tm_1; 1.
 DR PROSITE: PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL2; 1.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 216 216
 SQ SEQUENCE 216 AA; 23963 MW; FF89E278BD1D479F CRC64;

Query Match 68.3%; Score 1098; DB 4; Length 216;
 Best Local Similarity 99.5%; Pred. No. 1e-93;
 Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 68 LLDLCYTTCTVPQMLVNLCSIRKVISYRGCAVLFLALGATEYLLAVMSFDMWPAIC 127
 DB 1 LLDLCYTTCTVPQMLVNLCSIRKVISYRGCAVLFLALGATEYLLAVMSFDMWPAIC 60
 QY 128 RPLHYVIMQRLCLQLAASWYTGFSNSWMLSTLTQLPLCDPYVDHFLCEVPALLK 187
 DB 61 RPLHYVIMQRLCLQLAASWYTGFSNSWMLSTLTQLPLCDPYVDHFLCEVPALLK 120
 QY 188 SCVETTANEAELELVSELFLHILPLTLILISYAFIVRAVLRIQSAEGKRAFGTCSHLIY 247
 DB 121 SCVETTANEAELELVSELFLHILPLTLILISYAFIVRAVLRIQSAEGKRAFGTCSHLIY 180
 QY 248 VSLFYSTAVSVYLOPPSPSSKDGKMWLSFYGIAP 283
 DB 1 VSLFYSTAVSVYLOPPSPSSKDGKMWLSFYGIAP 283

DB 181 VSLFYSTAVSVYLOPPSPSSKDGKMWLSFYGIAP 216
 RESULT 3
 ID 09GZK6 PRELIMINARY; PRT; 312 AA.
 AC 09GZK6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE OLFACTORY RECEPTOR
 GN 6M1-4P*05 OR 6M1-4P*02.
 GN Homo sapiens (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ziegler A., Ehlers A., Forbes S.A., Trowsdale J., Uchanska-Ziegler B.,
 RA Volz A., Younger R., Beck S.;
 RT "Polymorphic olfactory receptor genes and HLA loci constitute extended
 haplotypes."
 RL (In) Kasahara M. (eds.);
 RL MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION, STRUCTURE, AND FUNCTION,
 RL pp.110-130, Springer-Verlag, Tokyo, Japan (2000).
 DR EMBL: AJ302570; CAC20490.1; -;
 DR EMBL: AJ302565; CAC20485.1; -;
 DR EMBL: AJ302566; CAC20486.1; -;
 DR EMBL: AJ302569; CAC20489.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR00237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G_PROTEIN_RECEPTOR_FL1; UNKNOWN_1.
 DR PROSITE: PS50262; G_PROTEIN_RECEPTOR_FL2; 1.
 KW Receptor.
 SQ SEQUENCE 312 AA; 35454 MW; 0C08C09B2DBA4835 CRC64;

Query Match 57.1%; Score 917; DB 4; Length 312;
 Best Local Similarity 58.8%; Pred. No. 7.7e-77;
 Matches 177; Conservative 43; Mismatches 81; Indels 0; Gaps 0;
 QY 5 NDSITIDEFILLGSDRPMLEFLLVFLSYTYTGNGLTITILVSRIDTYLHPMWFELT 64
 DB 6 NASFEDEFILLGFSNMPHELVFLVLLITLGNELIILSYDSHLHPMWFELT 65
 QY 65 NLSLDLCYTTCTVPQMLVNLCSIRKVISYRGCAVLFLALGATEYLLAVMSFDMWPAIC 124
 DB 66 NLSFDLCYTTSSIPQMLVNLGPEKTIYAGCTVOLFLVLAIGTACVLLVMSFDRIA 125
 QY 125 AICRPLHYVIMQRLCLQLAASWYTGFSNSWMLSTLTQLPLCDPYVDHFLCEVPAL 184
 DB 126 AICRPLHYVIMQRLCLQLAASWYTGFSNSWMLSTLTQLPLCDPYVDHFLCEVPAL 185
 QY 185 LKLSCEVTANEAELELVSELFLHILPLTLILISYAFIVRAVLRIQSAEGKRAFGTCSHLIY 244
 DB 186 LKLSCEVTANEAELELVSELFLHILPLTLILISYAFIVRAVLRIQSAEGKRAFGTCSHLIY 245
 QY 245 LIYVSLFYSTAVSVYLOPPSPSSKDGKMWLSFYGIAPMLNPLIYLRNKEVKEGFKRL 304
 DB 246 LIYVSLFYSTAVSVYLOPPSPSSKDGKMWLSFYGIAPMLNPLIYLRNKEVKEGFKRL 305
 QY 305 V 305
 DB 306 M 306
 RESULT 4
 ID 09GZK1 PRELIMINARY; PRT; 312 AA.
 AC 09GZK1;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)

Query Match	55.5%;	Score 892;	DB 11;	Length 302;
Best Local Similarity	56.9%;	Pred. No. 1.5e-74;		
Matches 174;	Conservative 48;	Mismatches 76;	Indels 8;	Gaps 2.

[illegible]

RESULT	7
Q9WV11	
Q9WV11	PRELIMINARY; PRT; 312 AA.
AC	Q9WV11;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE	573k1.8 (MM17M1-2 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY (OLEFACTORY RECEPTOR LIKE) PROTEIN))).
GN	GABBR1 OR 573K1.8.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RA	SEQUENCE FROM N.A.
RP	Younger R.;
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AL078630; CAB45000.1; --
DR	MGI: MGI1860139; GABDr1.
DR	Interpro: IPR000276; GPCR_Rhodpsn.
DR	Pfam: PF00001; 7tm_1.1.
DR	PRINTS: PRO0237; GPCRHHODPSN.
DR	PROSITE: PS00237; G_PROTEIN_RECP_FL_1; UNKNOWN_1.
KW	PROSITE: PS50262; G_PROTEIN_RECP_FL_2; 1.
Q0	RECEPTOR; Transmembrane.
Q0	SEQUENCE 312 AA; 34786 MW; DAA7507C7771AD8 CRC64;

Query Match	54.8%;	Score 881;	DB 11;	Length 312;
Best Local Similarity	55.6%;	Pred. No. 1.6e-73;		
Matches 169;	Conservative 49;	Mismatches 86;	Indels 0;	Gaps 0;

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QY 4 VNDSIQEIIILGSDRNMLEFFLLVFLISYTTITGINLTIILVSRDRLKHPMFFL 63
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 VNOSPVGEFLLIGSEHQLEKRVLEVVVLCYLLTLTGNTLITLLSLDPLRSPMFFL 61
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 64 TNLSLDLDCYTTCTVCPQMLIVMLCSIRKIVSYRCVAOLETFLGATEYLLAWSEDFE 123
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SNLSRLDCLFTTTCVPQMLRFLMGPRTKTIISPLGGSVOLFIMLLGTTBECILLTMARDRY 122
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 124 VAICRPLHYSVIIMHOKLCLOLAAASWVTGFSNSVWLSTLTQLPLCDPYVIDHLECEVA 183
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db	122	VAVOQPLHYATIIHPRICRQIAGVAMMIGLVQSTVOIPLPTLPEFCSHRQIDDFLCEVPS	181
Qy	184	LKLSCEVTTANAEDELVLVSEFLHLPLTLTLISYAFIVRAVLRISQAEGRQAFGTCS	243
Dv	182	LIRSCGDTFNEIQLSAGVIGELFVPLSLIIYSYGVIAARVATKNTSSKRRRNFGTCS	241
Qy	244	HLIVSLFYSTNAVSVIYIQPPSPSSKDDGKNMSLFYGIILAPLNPLIYTLLNKKEVKEGFKR	303
Dv	242	HLIVTTFEYSVIAVVIYIQPKNPYAQERSKEGFLFYAVAGTLPNLVYTLNKKVEYKRAFWR	301
Qy	304	LVAR	307
Dv	302	LLGK	305

RESULT	8		
Q9R0Z2			
ID	Q9R0Z2	PRELIMINARY:	PRT: 312 AA.
AC	Q9R0Z2;		
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, last sequence update)		
DT	01-JUN-2001 (TrEMBLrel. 17, last annotation update)		
DE	573k1.3 (MM17M1-4 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY)		
DE	(GOLFACTORY RECEPTOR LIKE) PROTEIN)).		
GN	GABBR1 OR 573K1.3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID:10090;		
RN	[1]		
RA	SEQUENCE FROM N.A.		
RP	Younger R.;		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: A0078630; CAB4495.1; -.		
DR	MGI:1860139; Gabbit.		
DR	Interpro: IPR000276; GPCR_Rhodopsn.		
DR	Pfam: PF00001; 7tm1.1, 1.		
DR	PRINTS: PR00237; GPCRHHODPSN.		
DR	PROSITE: PS00237; G_PROTEIN_REC_P1.1; UNKNOWN_1.		
DR	PROSITE: PS50262; G_PROTEIN_REC_P1_2; 1.		
DR	Receptor: Transmembrane.		
Q0	SEQUENCE 312 AA; 34999 MW; 83374B1A4C6F912D CRC64;		

Query Match	54.38;	Score 872;	DB 11;	Length 312;
Best Local Similarity	55.68;	Pred. No. 1.1e-72;		
Matches 169;	Conservative 51;	Mismatches 84;	Indels 0;	Gaps 0;

OY	4	VNDSDIOEFLIGSDRPMLEFFRLVVEILSVYUIGENLILIVSLDOKTKLPMFEFL	63
Db	2	VN0SSPVEFLIGRSEHQLEKVLVFIVLCSYLLTLGNTLILLLSTDLRHLN5PMFEFL	61
OY	64	TNLSLIDLCYTTCTVPOMLVNLCSIKRVIYSIRGVADOLFPLMAGATEYLLAVMSDFM	1233
Db	62	SNLSFLDCFTYTTVPOLFLNLMSPATISFLGCSVGLFPLSGTTECLLILVMSDRY	121
OY	124	VAISRPILHYSYIMHQRCLDLOLAASWVTGSENSVWLSLTLDLPYIDHFLCEVPA	1833
Db	122	VAVQPLHYATVHPRICOMKLAAYAMMGLI05VQRPRLTKLPECRH9IDDFLCEVPS	181
OY	184	LKLSCEVTTANEAEFLVSLFHLRLPLTLILISATIVARVLRIG0ABEGR0KAFGCGS	2433
Db	182	LIRLSGGETTNEILQLVAVSVYLAVVPSLISVSGAIAARVMIINSTEYMKAKALFRCCS	2411
OY	244	HLIVSLFEPAVSVLYLOPSPSSKDDGKMVSLFYGIIAPMLPILTLNKKVEKEGFKR	3033
Db	242	HLIVTLFEYSVIAVLIQPKNPYAOERKGKFGFLFYAVGFTPLNPLILTLNKKVEKRAFMR	301
OY	304	LVAR 307	
Db	302	LLGR 305	


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Db 1 MPTNESHPEEFILGADPWLLEPLFTSLIMYPIAVNGNTIILMSRLDSLSPMY 60
QY 61 FFLTNLSLDLCYTCCTVPPOMLVNLCIRKIVISRGCAVOLFIALGATEYLLAAVMSF 120
Db 61 FFLTNLSLDLCYTCCTVPPOMLVNLCIRKIVISRGCAVOLFIALGATEYLLAAVMSF 120
QY 121 DMFVAICRPLHYSVIMHQRCLQL--AAASW-----VTFNSVWLSLTTL 164
Db 121 DMFVAICRPLHYSVIMHQRCLQL--AAASW-----VTFNSVWLSLTTL 164
QY 121 DRYVAICRPLHYTLIMNQRVCIISEFHRVANMNNLCRLGHCHITIAVCSNK----- 172
Db 121 DRYVAICRPLHYTLIMNQRVCIISEFHRVANMNNLCRLGHCHITIAVCSNK----- 172
QY 165 QLEPLCDPYVDHFLCEYFPAALKSCVETANEAEFLVSEFLHILPTLLISTAFIVRA 224
Db 165 QLEPLCDPYVDHFLCEYFPAALKSCVETANEAEFLVSEFLHILPTLLISTAFIVRA 224
QY 173 -----LDHVCETIPVLIKTIACGKSGNETLSVVCIFMLAVPLCLTLASVATGSA 223
Db 173 -----LDHVCETIPVLIKTIACGKSGNETLSVVCIFMLAVPLCLTLASVATGSA 223
QY 225 VLRIASAEGROKAFGTCGSHLIVSLFYSTAVSYIOLPPSSSKDOGKWSLFGIITAPM 284
Db 225 VLRIASAEGROKAFGTCGSHLIVSLFYSTAVSYIOLPPSSSKDOGKWSLFGIITAPM 284
QY 224 VFKIKSSKGRKKAFCGTCSSHLIVFLFYGPATSMYLOPPSSISRDPKFMALFYGVYTPS 283
Db 224 VFKIKSSKGRKKAFCGTCSSHLIVFLFYGPATSMYLOPPSSISRDPKFMALFYGVYTPS 283
QY 285 LNPLIYTLRNKVEYEGEGRVLVARY 308
Db 285 LNPLIYTLRNKVEYEGEGRVLVARY 308
QY 284 LNPFITYTLRNKNVKGALRNLVRSI 307
Db 284 LNPFITYTLRNKNVKGALRNLVRSI 307

RESULT 12
Q92022
ID 092022 PRELIMINARY; PRT; 318 AA.
AC 092022;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE B7 OLFACTOR RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
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RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
DR EMBL; AF321234; AAK84169.1; -.
KW Receptor.
SQ SEQUENCE 318 AA; 35150 MW; E9A182AEA21BSCAO CRC64;

Query Match 49.9%; Score 802; DB 11; Length 318;
Best Local Similarity 51.1%; Pred. No. 3.3e-66;
Matches 158; Conservative 58; Mismatches 91; Indels 2; Gaps 2;
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RESULT 13
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DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE B2 OLFACTOR RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ;
RX MEDLINE=21310002; PubMed=11416212;
RA Lane R.P., Cutforth T., Young J., Athanasiou M., Friedman C.,
RA Rowen L., Evans G., Axel R., Hood L., Trask B.J.;
RT "Genomic analysis of orthologous mouse and human olfactory receptor
RT loci."
RL Proc. Natl. Acad. Sci. U.S.A. 98:7390-7395(2001).
DR EMBL; AF321233; AAG45183.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR InterPro: IPR000478; TNF_family.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS00251; TNF_1; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 314 AA; 35154 MW; 6325415D032FCD1B CRC64;

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Best Local Similarity 51.8%; Pred. No. 2.2e-65;
Matches 158; Conservative 54; Mismatches 91; Indels 2; Gaps 1;

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Db 4 NQQTVEFILLGSDDDHTOKLFLFLGYMTVGLNLMFLVRSRLHPMYEFLC 63
QY 65 NLSLDLCYTCCTVPPOMLVNLCIRKIVISRGCAVOLFIALGATEYLLAAVMSFDFV 124
Db 64 NLSLDLCYTCCTVPPOMLVNLCIRKIVISRGCAVOLFIALGATEYLLAAVMSFDFV 123
QY 125 AICRPLHYSVIMHQRCLQLAAASWVTGFSNSVWLSLTTLQPLCDPYVDHFLCEVPAL 184
Db 124 AICNPLHYSIMHQRVCIQATVSWTGIIVSVDTFTFLRLPGRGNSIAHFCEAPAL 183
QY 185 LKLSCEVTANEAEFLVSEFLHILPTLLISYAFIVRAVLRIOASGROKAFGTCGSH 244
Db 184 LKLSADCTQSEAMVFLMGVLLITIPVSLIVSGHITIVVKKMSAAGRKASTGSH 243
QY 245 LIIVSLFYSTAVSYIOLPPSSSKDOGKWSLFGIITAPMLNPLIYTLRNKVEYEGFRK 304
Db 244 LMVILFYGSAIITYMP--KSKKEGKLVSVFAMVTPMLNPLIYTLRNKVDYKGLMKV 301
QY 305 VAVVF 309
Db 302 AMKNF 306

RESULT 14
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ID 09EPG6 PRELIMINARY; PRT; 314 AA.
AC 09EPG6;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 18:24:47 ; Search time 3373.42 Seconds

(without alignments)
6047.782 Million cell updates/sec

Title: US-09-800-321A-3

Perfect score: 943

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2	940.4	99.7	993	31	US-09-800-321a-1			Sequence 1, App11			
3	940.4	99.6	113710	64	US-60-258-250-40			Sequence 40, App1			
4	938.8	99.6	942	29	US-09-755-017-1			Sequence 1, App1			
5	938.8	99.6	1488	29	US-09-755-017-3			Sequence 3, App11			
6	937.2	99.4	956	31	US-09-800-321a-5			Sequence 5, App11			
7	716.8	76.0	20410	65	US-60-261-976-77			Sequence 77, App1			
8	665.2	70.5	1047	75	US-60-360-207-43515			Sequence 43515, A			
9	602.2	63.9	1071	75	US-60-360-207-42178			Sequence 604, App			
10	600.4	63.7	673	56	US-60-178-308-604			Sequence 604, App			
11	534	56.6	46924	63	US-60-245-225-86			Sequence 86, App1			
12	534	56.6	46924	64	US-60-258-250-27			Sequence 27, App1			
13	534	56.6	68666	63	US-60-248-505-274			Sequence 274, App			
14	529.4	56.1	1510	63	US-60-248-505-1606			Sequence 1606, App			
15	505.6	53.6	642	55	US-60-162-248-93			Sequence 93, App1			
16	505.6	53.6	642	55	US-60-162-232-238			Sequence 238, App			
17	505.6	53.6	642	55	US-60-163-232-238			Sequence 238, App			
18	505.6	53.6	642	55	US-60-169-842-1245			Sequence 1245, App			
19	486.4	51.6	488	56	US-60-178-308-697			Sequence 697, App			
20	484.4	47.6	1324	63	US-60-245-225-556			Sequence 556, App			
21	448.4	47.6	1324	64	US-60-258-250-167			Sequence 167, App			
22	448	47.5	2940	24	US-09-634-306B-111618			Sequence 111618, App			
23	426	45.2	438	57	US-60-186-652-484			Sequence 484, App			
24	406.8	43.1	1037	34	US-09-924-359-3			Sequence 3, App11			
25	406.8	43.1	1037	34	US-09-924-359-5			Sequence 5, App11			
26	403.6	42.8	939	1	PCT-US01-07771-26			Sequence 26, App1			
27	403.6	42.8	939	1	PCT-US01-20122-26			Sequence 26, App1			
28	403.6	42.8	939	31	US-09-804-291-26			Sequence 26, App1			
29	403.6	42.8	939	37	US-09-886-055-26			Sequence 26, App1			
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31	403.6	42.8	998	34	US-09-924-359-1			Sequence 1, App1			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Yu, M.
09/1800321
Seq. IDs 34 w/
Interf

32	402	12.6	939	59	US-60-360-222-19	Sequence 19, Appl
33	383.2	40.6	948	75	US-60-360-207-43111	Sequence 43111, A
34	371.6	39.4	948	26	US-09-667-889-4	Sequence 4, ApplII
35	371.6	39.4	948	36	US-09-378-525-4	Sequence 4, ApplII
36	371.6	39.4	1005	37	US-10-034-842-1	Sequence 1, ApplII
37	371.6	39.4	1500	37	US-10-034-842-3	Sequence 3, ApplII
38	370	39.2	971	34	US-09-912-976-19	Sequence 19, Appl
39	370	39.2	1005	1	PCT-US01-07771-1.366	Sequence 366, App
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42	370	39.2	1005	33	US-09-886-055-366	Sequence 366, App
43	370	39.2	1065	19	US-09-524-730-7	Sequence 7, ApplII
44	370	39.2	1065	37	US-10-028-521-7	Sequence 7, ApplII
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ALIGNMENTS

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RESULT 1
US-09-800-321A-3
: Sequence 3, Application US/09800321A
: GENERAL INFORMATION:
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Burgess, Catherine E
: APPLICANT: Mishra, Vishnu
: APPLICANT: Li, Li
: APPLICANT: Baumgartner, Jason C
: APPLICANT: Majumder, Kumud
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Tchiernev, Vasilair T
: TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 15966-703 US
: CURRENT APPLICATION NUMBER: US/09/800,321A
: CURRENT FILING DATE: 2001-03-05
: PRIOR APPLICATION NUMBER: 60/186,606
: PRIOR FILING DATE: 2000-03-03
: PRIOR APPLICATION NUMBER: 60/221,942
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: 60/260,285
: PRIOR FILING DATE: 2001-01-08
: PRIOR APPLICATION NUMBER: 60/220,263
: PRIOR FILING DATE: 2000-07-24
: PRIOR APPLICATION NUMBER: 60/257,600
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/187,295
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/189,854
: PRIOR FILING DATE: 2000-07-21
: PRIOR APPLICATION NUMBER: 60/187,249
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/187,247
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/187,250
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/187,253
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/187,248
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/187,296
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/187,563
: PRIOR FILING DATE: 2000-03-07
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 943
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-800-321A-3

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Query Match	100.08;	Score 943;	DB 31;	Length 943;
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Best Local Similarity 100.0%; Pred. No. 1.4e-273;
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; Sequence 1, Application US/09800321A
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara

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1  APPLICANT: Burgess, Catherine E
2  APPLICANT: Mishra, Vishnu
3  APPLICANT: Li, Li
4  APPLICANT: Baumgartner, Jason C
5  APPLICANT: Majumder, Kumud
6  APPLICANT: Spytek, Kimberly A
7  APPLICANT: Tchernev, Veltzar T
8  TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
9  FILE REFERENCE: 15966-703 US
10 CURRENT APPLICATION NUMBER: US/09/800,321A
11 PRIOR FILING DATE: 2001-03-05
12 PRIOR APPLICATION NUMBER: 60/186,606
13 PRIOR FILING DATE: 2000-03-03
14 PRIOR APPLICATION NUMBER: 60/221,942
15 PRIOR FILING DATE: 2000-07-31
16 PRIOR APPLICATION NUMBER: 60/260,285
17 PRIOR FILING DATE: 2001-01-08
18 PRIOR APPLICATION NUMBER: 60/220,263
19 PRIOR FILING DATE: 2000-07-24
20 PRIOR APPLICATION NUMBER: 60/257,600
21 PRIOR FILING DATE: 2000-12-21
22 PRIOR APPLICATION NUMBER: 60/187,295
23 PRIOR FILING DATE: 2000-03-06
24 PRIOR APPLICATION NUMBER: 60/219,854
25 PRIOR FILING DATE: 2000-07-21
26 PRIOR APPLICATION NUMBER: 60/187,249
27 PRIOR FILING DATE: 2000-03-06
28 PRIOR APPLICATION NUMBER: 60/187,247
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31 PRIOR FILING DATE: 2000-03-06
32 PRIOR APPLICATION NUMBER: 60/187,253
33 PRIOR FILING DATE: 2000-03-06
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35 PRIOR FILING DATE: 2000-03-06
36 PRIOR APPLICATION NUMBER: 60/187,236
37 PRIOR FILING DATE: 2000-03-06
38 PRIOR APPLICATION NUMBER: 60/187,563
39 PRIOR FILING DATE: 2000-03-07
40 NUMBER OF SEQ ID NOS: 78
41 SOFTWARE: PatentIn Ver. 2.1
42 SEQ ID NO 1
43 LENGTH: 993
44 TYPE: DNA
45 ORGANISM: Homo sapiens
46 US-09-800-321A-1

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Db	255 atgcagtaaaattttatgcagcactcaggaagaagaatcagattatccgtgctgttaagccag	314			
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Db	315	ctcttcacattccgagctcgggagcgtacacgaatactctcccgagcgcaagctctct	374
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Qy	422	tgctctccagttggcagagctgcacatcctctggtgttaactggttttgtaaccagtggtgtgtct	481
Db	435	tgccctccagttggcagagctgcacatcctctggtgttaactggttttgtaaccagtggtgtgtct	494
Qy	482	aacctgaactccacagctgcacactctgagaccccatgtgatacatcctctctctgtgaa	541
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Qy	602	cttgtaacatgagctctccatctaataccctgtgacacatcccttatcatatgtcttt	661
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Db	735	tgtgtgtcccatcctaattgtgtgtctctcttttttatgatgcgaagcgctctgtgtgacctg	794
Qy	782	caacacacttcgcccagctctccaaagacccaagaaagatgttctctctctctatgtgaatc	841
Db	795	caacacacttcgcccagctctccaaagacccaagaaagatgttctctctctctatgtgaatc	854
Qy	842	attgacacactgcgtgaatccctctatatatacaactttagagacaaaggggtcaaaaggaagc	901
Db	855	attgacacacactgcgtgaatccctctatatatacaactttagagacaaaggggtcaaaaggaagc	914
Qy	902	tttaaaaggttggttgcaagaagctctccttaatacaagaataaa	943
Db	915	tttaaaaggttggttgcaagaagctctccttaatacaagaataaa	956

```

      RESULT 3
      US-60-258-250-40/c
      ; Sequence 40, Application US/60258250
      ; GENERAL INFORMATION:
      ; APPLICANT: Beasley, Ellen
      ; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
      ; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
      ; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
      ; FILE REFERENCE: CLO01035-PROV
      ; CURRENT APPLICATION NUMBER: US/60/258.250
      ; CURRENT FILING DATE: 2000-12-27
      ; NUMBER OF SEQ ID NOS: 210
      ; SOFTWARE: FastSeq for Windows Version 4.0
      ; SEQ ID NO 40
      ; LENGTH: 113710
      ; TYPE: DNA
      ; ORGANISM: HUMAN
      US-60-258-250-40

      Query Match          99.7%;      Score 940.4;  DB 64;      Length 113710;
      Best Local Similarity 99.9%;      Pred. No. 8.6e-272;
      Matches 941; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

      QY      2      atgaattgggttaagacgaagcgtctacaagaagttattctgctggtgtcttcagatcga 61
      |||||||
      Db      91948  atgaaattgggtaaatgacagacatcattacaagagattattctgctggtgtcttcagatcga 91889
      |||||||
      QY      62      ccttgctgaagttcccaactccttctgtgctctcttgaattcttacaacgtgacacattt 121

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Db	91888	CGTTGGCTGGAATTTCACACTCCTTGTGGCTCTTGGATTTCCTTAACACTGTGACCAATCTTT	918229
Qy	122	ggcaatctcgaccatlatlcttagtgcagcgcctgcagacaccaatcatalaccacca tgc	181
Db	91828	GGCAATCTGACCAATTATTTCTAGTGTGACAGCCCTGGACACCAAACTTCATTAACCCCATGTAT	917659
Qy	182	tttttcttaccaatctatcaetctctgtgactcttctgttaacacatatgacgtccacaa	241
Db	91768	TTTTTTCTTTACCAACTATACACTCCCTGGATCTTTGTATACACCACTATACACTCCACAA	917099
Qy	242	atgcagtaaatattatgcagcatgaagaaatcaagatcatcgtggtcgtgttagccag	301
Db	91708	ATGCTATGTAATTTATGACGATCAGGAAGTAATCAGTTATCTGTGTGTGTATGCGCTGTATGCCAG	91649
Qy	302	ctttcatacttctctgaccttggggcctaacatgatatctctctctgcgcgtcatgtccctt	361
Db	91648	CTTTTCATATTTCTGGCCCTTGGGGGCTACTGAATATCTCTCTCTGCGCTCATGTCTTT	91589
Qy	362	gattggtttgtatgcattttgtcgcctctcatctatcagttatcatatgcacagagactc	421
Db	91588	GATAGGTTTGTATGCTATTTGTGTGGCCCTCCATTACTCAGTTATCATATGACACAGAGACTTC	91529
Qy	422	tcccacagtttggagcgtgcgactcccggtttactggttttagtaactgaagtgtgtgct	481
Db	91528	TCCCTTCAGTTTGACGCTGCACTCTGGGTTACTGTGTTAGTATCACTCAAGTGTGTGTCT	91469
Qy	482	accctgaactctcagactgcgcactctgtgacccctatgtatagatcaacttctcgtga	541
Db	91468	ACCCGACCTCTCCACTGCGACACTCTGTGACACCCCTATGTATGATGATCACTTCTCTGTGA	91409
Qy	542	gtccctgcagctgcctcaagttatcttctgtgttgagacaaacagcaaatgagctgaactatlc	601
Db	91408	GTCCCTGCACTGCTCAAGTTATCTGTGTGTGAGACAACAGCAAAATGAGGCTGAATATTC	91349
Qy	602	cttgcagtgagctcttcatatctaatacccccgaacctcatctctatatcatatgctttt	661
Db	91348	CTTGTGACGAGACTCTTCCATCTAATATACCCCTGACACATCACTCTTAATATCATATGCTTTT	91289
Qy	662	attgcgcagcagatattgaggaatacagtcgtctgaagtgcgacaaagaacatttggaga	721
Db	91288	ATTGTGCCAGGAGATATGAGATATACAGTCTGCTGAAGTCCGACAAAMACATTTGGACA	91229
Qy	722	tgtgttcccatctaatgtgtgtgtctcttlttataagtagtacagcgcgtctgtgtacbtg	781
Db	91228	TGTGTTTCCCATCTAATATGTGTGTCTCTTTTATATGACAGCCGTCCTGTATACCG	91169
Qy	782	caaccaacttgcgccagctccaaggaaccaagaaagatgttctctctctctatgaaac	841
Db	91168	CAACACACTCTCCCGACGCTCCCAAGACCAAGAAAGATGTCTCTCTTATATGAAATC	91109
Qy	842	attgcacccatgttaatcccttatataatacatttagaagaaagagtagaagaagc	901
Db	91108	ATTGCACCCATGCTTAATCCCTTATATATACACTTAGAACAAGAGAGTAAGGAAGC	91049
Qy	902	tttaaaagttgtgtcagaagtlcttcttaalcaagaataa	943
Db	91048	TTTAAAGGTGTGTGCAAGACTTCTTTAATCAAGAAATAA	91007
RESULT 4			
US-09-755-017-1			
: Sequence 1, Application US/09755017			
: GENERAL INFORMATION:			
: APPLICANT: Walke, D. Wade			
: APPLICANT: Wilganowski, Nathaniel			
: APPLICANT: Turner, C. Alexander Jr.			
: APPLICANT: Friedrich, Glenn			
: APPLICANT: Abouin, Alejandro			
: APPLICANT: Zambrowicz, Brian			
: APPLICANT: Sands, Arthur T.			
: TITLE OF INVENTION: Novel Human Membrane Proteins and			
: TITLE OF INVENTION: Polynucleotides Encoding the Same			

```

; FILE REFERENCE: LEX-0115-USA
; CURRENT APPLICATION NUMBER: US/09/755,017
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 60/175,764
; PRIOR FILING DATE: 2000-01-12
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-755-017-1

Query Match      99.6%;      Score 938.8;  DB 29;      Length 942;
Best Local Similarity 99.8%;      Pred. No. 2.6e-272;
Matches 940; Conservative 0; Mismatches 2; Indels 0; Gaps 0

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QY 842 attgcacccatgtctgaatcccttataatacaactaggacaaggagtaagaagc 901
 |||
 Db 841 atgcacccatgtctgaatcccttataatacaactaggacaaggagtaagaagc 900
 QY 902 tttaaaaggttggttcgaagagttcttcaatcaagaataa 943
 |||
 Db 901 tttaaaaggttggttcgaagagttcttcaatcaagaataa 942

RESULT 5
 US-09-755-017-3

Sequence 3, Application US/09755017
 GENERAL INFORMATION:
 APPLICANT: Walke, D. Wade
 APPLICANT: Milgowski, Nathaniel
 APPLICANT: Turner, C. Alexander Jr.
 APPLICANT: Friedrich, Glenn
 APPLICANT: Abuin, Alejandro
 APPLICANT: Zambrowicz, Brian
 APPLICANT: Sands, Arthur T.
 TITLE OF INVENTION: Novel Human Membrane Proteins and
 TITLE OF INVENTION: Polynucleotides Encoding the Same
 FILE REFERENCE: LEX-0115-USA
 CURRENT APPLICATION NUMBER: US/09/755,017
 PRIOR FILING DATE: 2001-01-05
 PRIOR APPLICATION NUMBER: US 60/175,764
 NUMBER OF SEQ ID NOS: 3
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 1488
 TYPE: DNA
 ORGANISM: Homo Sapien
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1488)
 OTHER INFORMATION: n = A,T,C or G
 US-09-755-017-3

Query Match 99.6%; Score 938.8; DB 29; Length 1488;
 Best Local Similarity 99.8%; Pred. No. 3.3e-272;
 Matches 940; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgaattgggttaaatgacagcatalacagagattatctgctgggttctcagatcga 61
 |||
 Db 198 atgaattgggttaaatgacagcatalacagagattatctgctgggttctcagatcga 257
 QY 62 ccttgctgaggttccactccttggtgctcttgaattcttcaactgtgacatcctt 121
 |||
 Db 258 ccttgctgaggttccactccttggtgctcttgaattcttcaactgtgacatcctt 317
 QY 122 ggcacatcagcatatctagtgtcagcccttgacacacaaattatccccatgat 181
 |||
 Db 318 ggcacatcagcatatctagtgtcagcccttgacacacaaattatccccatgat 377
 QY 182 tttttcttcaacatcatcactcctggtcttgtttaaccacatgtaagtcaccaa 241
 |||
 Db 378 tttttcttcaacatcatcactcctggtcttgtttaaccacatgtaagtcaccaa 437
 QY 242 atgctagttaattatgacagcatcaagaaagtaatcaagtatctgtgtgtagccag 301
 |||
 Db 438 atgctagttaattatgacagcatcaagaaagtaatcaagtatctgtgtgtagccag 497
 QY 302 ctttcaatttttgcttgctgggaggtactgaatcttctctggccgcatgctctt 361
 |||
 Db 498 ctttcaatttttgcttgctgggaggtactgaatcttctctggccgcatgctctt 557
 QY 362 gatgtgtgtgtagctattgtgctgcttccatattacagttatcaatgacacagactc 421
 |||
 Db 558 gatgtgtgtgtagctattgtgctgcttccatattacagttatcaatgacacagactc 617

QY 422 tgcctcagttggtcagatcctctgtgttaactggttttagtaactcagtggtgtct 481
 |||
 Db 618 tgcctcagttggtcagatcctctgtgttaactggttttagtaactcagtggtgtct 677
 QY 482 accctgactcagctgacacactctgtgacccctatgtagatcaactctctgtgaa 541
 |||
 Db 678 accctgactcagctgacacactctgtgacccctatgtagatcaactctctgtgaa 737
 QY 542 gtccctgacatgtctcaagtatctgtgtgagacaacaagaaatgaggtgaacttc 601
 |||
 Db 738 gtccctgacatgtctcaagtatctgtgtgagacaacaagaaatgaggtgaacttc 797
 QY 602 ctgtgtagtgagctcttccatcttaataccctgtaactatccttataatgtctt 661
 |||
 Db 798 ctgtgtagtgagctcttccatcttaataccctgtaactatccttataatgtctt 857
 QY 662 atgtccgagcagatctgaagatagacagctgctggaagtgacaaagaattgggaca 721
 |||
 Db 858 atgtccgagcagatctgaagatagacagctgctggaagtgacaaagaattgggaca 917
 QY 722 tgtgttcccatctaatgtgtgtctcttlttataagtaacagcgtctctgtgacctg 781
 |||
 Db 918 tgtgttcccatctaatgtgtgtctcttlttataagtaacagcgtctctgtgacctg 977
 QY 782 caaccaccttgcccgatctccaagagccaagaaagatgttctctctctatgtaac 841
 |||
 Db 978 caaccaccttgcccgatctccaagagccaagaaagatgttctctctctatgtaac 1037
 QY 842 atgcacccatgtctgaatcccttataatacaactttagagacaaggagtaagaagc 901
 |||
 Db 1038 atgcacccatgtctgaatcccttataatacaactttagagacaaggagtaagaagc 1097
 QY 902 tttaaaaggttggttcgaagagttcttcaatcaagaataa 943
 |||
 Db 1098 tttaaaaggttggttcgaagagttcttcaatcaagaataa 1139

RESULT 6
 US-09-800-321A-5

Sequence 5, Application US/09800321A
 GENERAL INFORMATION:
 APPLICANT: Padigaru, Murallidhara
 APPLICANT: Burgess, Catherine E
 APPLICANT: Mishra, Vishnu
 APPLICANT: Li, Li
 APPLICANT: Baumgartner, Jason C
 APPLICANT: Majumder, Kumud
 APPLICANT: Spytek, Kimberly A
 APPLICANT: Tchernev, Velizar T
 TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
 FILE REFERENCE: 15966-703 US
 CURRENT APPLICATION NUMBER: US/09/800,321A
 PRIOR FILING DATE: 2001-03-05
 PRIOR APPLICATION NUMBER: 60/186,606
 PRIOR FILING DATE: 2000-03-03
 PRIOR APPLICATION NUMBER: 60/221,942
 PRIOR FILING DATE: 2000-07-31
 PRIOR APPLICATION NUMBER: 60/260,285
 PRIOR FILING DATE: 2001-01-08
 PRIOR APPLICATION NUMBER: 60/220,263
 PRIOR FILING DATE: 2000-07-24
 PRIOR APPLICATION NUMBER: 60/257,600
 PRIOR FILING DATE: 2000-12-21
 PRIOR APPLICATION NUMBER: 60/187,295
 PRIOR FILING DATE: 2000-03-06
 PRIOR APPLICATION NUMBER: 60/219,854
 PRIOR FILING DATE: 2000-07-21
 PRIOR APPLICATION NUMBER: 60/187,249
 PRIOR FILING DATE: 2000-03-06
 PRIOR APPLICATION NUMBER: 60/187,247
 PRIOR FILING DATE: 2000-03-06
 PRIOR APPLICATION NUMBER: 60/187,250
 PRIOR FILING DATE: 2000-03-06

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; PRIOR APPLICATION NUMBER: 60/187, 253
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187, 248
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187, 296
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187, 563
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 956
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-800-321a-5
```

```
Query Match 99.4%; Score 937.2; DB 31; Length 956;
Best Local Similarity 99.7%; Pred. No. 8.1e-272;
Matches 939; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 atgaattggtaaatgacagacatcacatagaagattatctgctggtttctcagatcga 61
   |||||||
Db 7 atgaattggtaaatgacagacatcacatagaagattatctgctggtttctcagatcga 66
   |||||||

QY 62 ccttggtgagtttccactccttggcttctcttgattcttaccactgtgacatctt 121
   |||||||
Db 67 ccttggtgagtttccactccttggcttctcttgattcttaccactgtgacatctt 126
   |||||||

QY 122 ggaatcagacatttcttaagtgaagctgtgacacccaattatccccatgat 181
   |||||||
Db 127 ggaatcagacatttcttaagtgaagctgtgacacccaattatccccatgat 186
   |||||||

QY 182 ttttcttaccatcatcacctcgtgacattgtttaccacacatgtatgccacaa 241
   |||||||
Db 187 ttttcttaccatcatcacctcgtgacattgtttaccacacatgtatgccacaa 246
   |||||||

QY 242 atgctagttaattatgacagatcagaagaagtaatacagttatcgtgctgtgagccag 301
   |||||||
Db 247 atgctagttaattatgacagatcagaagaagtaatacagttatcgtgctgtgagccag 306
   |||||||

QY 302 ctttcatattcttgcccttgaggggcgaatgaatcttctcctggccgcatgtcctt 361
   |||||||
Db 307 ctttcatattcttgcccttgaggggcgaatgaatcttctcctggccgcatgtcctt 366
   |||||||

QY 362 gatctggtttgtagactatttggctgacctccatctactcagttatcattgacacagagatc 421
   |||||||
Db 367 gatctggtttgtagactatttggctgacctccatctactcagttatcattgacacagagatc 426
   |||||||

QY 422 tgcctcagttgagcagctgacatccctggttactggttttaagtaactcagtggtgtgtct 481
   |||||||
Db 427 tgcctcagttgagcagctgacatccctggttactggttttaagtaactcagtggtgtgtct 486
   |||||||

QY 482 accctgaactccagctgacagctgtgacacctatgtatgtatgatacacttctctgtga 541
   |||||||
Db 487 accctgaactccagctgacagctgtgacacctatgtatgtatgatacacttctctgtga 546
   |||||||

QY 542 gtccctgacagctgacagttatctgtgtgagacaacagcaaatgaggtgacatactc 601
   |||||||
Db 547 gtccctgacagctgacagttatctgtgtgagacaacagcaaatgaggtgacatactc 606
   |||||||

QY 602 ctgtgaatgagagcttctcactaataacccctgacactaactccttatatcatgtgttt 661
   |||||||
Db 607 ctgtgaatgagagcttctcactaataacccctgacactaactccttatatcatgtgttt 666
   |||||||

QY 662 attgtccgagcaatcatgagatagacagctgtcgtgaaggtgcacaanaaagcattgtggaca 721
   |||||||
Db 667 attgtccgagcaatcatgagatagacagctgtcgtgaaggtgcacaanaaagcattgtggaca 726
   |||||||

QY 722 tctgtgtcccatcaatactgtgtgtctctttttatagtaacagcgtctctgtgtacctgt 781
   |||||||
Db 727 tctgtgtcccatcaatactgtgtgtctctttttatagtaacagcgtctctgtgtacctgt 786
   |||||||
```

```
QY 782 caaccaccttcgccagctccacagacacgaagaagatgttctctctctatggaatc 841
   |||||||
Db 787 caaccaccttcgccagctccacagacacgaagaagatgttctctctctatggaatc 846
   |||||||

QY 842 atggcaccatctgtgatacccttatataataccttagagaagaagatgaagaagc 901
   |||||||
Db 847 atggcaccatctgtgatacccttatataataccttagagaagaagatgaagaagc 906
   |||||||

QY 902 tttaaaagtgtgtcgaagagcttcttctaatacaagaataca 943
   |||||||
Db 907 tttaaaagtgtgtcgaagagcttcttctaatacaagaataca 948
   |||||||
```

```
RESULT 7
US-60-261-976-77
; Sequence 77, Application US/60261976
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001089
; CURRENT APPLICATION NUMBER: US/60/261,976
; NUMBER OF SEQ ID NOS: 465
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77
; LENGTH: 20410
; TYPE: DNA
; ORGANISM: HUMAN
US-60-261-976-77
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Query Match 76.0%; Score 716.8; DB 65; Length 20410;
Best Local Similarity 86.3%; Pred. No. 1.5e-204;
Matches 815; Conservative 0; Mismatches 127; Indels 2; Gaps 2;
```

```
QY 2 atgaattggtaaatgacagacatcacatagaagattatctgctggtttctcagatcga 61
   |||||||
Db 1651 atgaattggtaaatgacagacatcacatagaagattatctgctggtttctcagatcga 1710
   |||||||

QY 62 ccttggtgagtttccactccttggcttctcttgattcttaccactgtgacatctt 121
   |||||||
Db 1711 ccttggtgagtttccactccttggcttctcttgattcttaccactgtgacatctt 1770
   |||||||

QY 122 ggaatcagacatttcttaagtgaagctgtgacacccaattatccccatgat 181
   |||||||
Db 1771 ggaatcagacatttcttaagtgaagctgtgacacccaattatccccatgat 1830
   |||||||

QY 182 ttttcttaccatcatcacctcgtgacattgtttaccacacatgtatgccacaa 241
   |||||||
Db 1831 ttttcttaccatcatcacctcgtgacattgtttaccacacatgtatgccacaa 1890
   |||||||

QY 242 atgctagttaattatgacagatcagaagaagtaatacagttatcgtgctgtgagccag 301
   |||||||
Db 1891 atgctagttaattatgacagatcagaagaagtaatacagttatcgtgctgtgagccag 1950
   |||||||

QY 302 ctttcatattcttgcccttgaggggcgaatgaatcttctcctggccgcatgtcctt 361
   |||||||
Db 1951 ctttcatattcttgcccttgaggggcgaatgaatcttctcctggccgcatgtcctt 2010
   |||||||

QY 362 gatctggtttgtagactatttggctgacctccatctactcagttatcattgacacagagatc 421
   |||||||
Db 2011 gatctggtttgtagactatttggctgacctccatctactcagttatcattgacacagagatc 2070
   |||||||

QY 422 tgcctcagttgagcagctgacatccctggttactggttttaagtaactcagtggtgtgtct 481
   |||||||
Db 2071 tgcctcagttgagcagctgacatccctggttactggttttaagtaactcagtggtgtgtct 2130
   |||||||

QY 482 accctgaactccagctgacagctgtgacacctatgtatgatacacttctctgtga 540
   |||||||
Db 2131 accctgaactccagctgacagctgtgacacctatgtatgatacacttctctgtga 2190
   |||||||
```



```

QY 541 agtccctgcactgctcaagtatctgtgttgagacaacagcaatgagctgactatt 600
DB 2191 agtccctgcactgctcaagtatctgtgttgagacaacagcaatgagctgactatt 2250
QY 601 ccttgtaagtgactctccatcaataaccccgacacatcccttatcatatgctt 660
DB 2251 ccttcacagtgactctccatcaataaccccgacacatcccttatcatatgctt 2310
QY 661 tatctgcagcagatattgagatacagctgtgaaagtcgacaaaagaattggag 720
DB 2311 tatctgcagcagatattgagatacagctgtgaaagtcgacaaaagaattggag 2370
QY 721 atgtgttcccatcaattgtgtgtctctttttatagacagcgctctgtgtaact 780
DB 2371 atgtgttcccatcaattgtgtgtctctttttatagacagcgctctgtgtaact 2430
QY 781 gcaacacacttcgcccagctcccaagacagaaagatgttctctctctatgtaac 840
DB 2431 gcaacacacttcgcccagctcccaagacagaaagatgttctctctctatgtaac 2490
QY 841 catlgaacacatgctgaatcccttatatacactaggaacaagaggtaaagagag 900
DB 2491 catlgaacacatgctgaatcccttatatacactaggaacaagaggtaaagagag 2550
QY 901 ctttaaaaggtgtgtgc-aagagctcttctaacaagaataa 943
DB 2551 ctttaaaaggtgtgtgc-aagagctcttctaacaagaataa 2594

RESULT 8
US-60-360-207-43515
; Sequence 43515, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360, 207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; LENGTH: 1047
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-43515

```

```

Query Match          70.5%; Score 665.2; DB 75; Length 1047;
Best Local Similarity 81.6%; Pred. No. 1.4e-189;
Matches 769; Conservative 0; Mismatches 173; Indels 0; Gaps 0;

QY 2 atgaattggtaaatgacagacatcaatacagagttatctgtctggtttctcagatcga 61
DB 106 atgaattggtaaatgacagacatcaatacagagttatctgtctggtttctcagatcga 165
QY 62 ccttgctgaggtttccacccctgtgtgtcttcttgaattcttcaactgtgacatcttt 121
DB 166 ccatgctgaggtttccacccctgtgtgtcttcttgaattcttcaactgtgacatcttt 225
QY 122 ggaacatctgacatcttactagtgatcagcctgagacccaacatctacacccatctat 181
DB 226 ggaacatctgacatcttactagtgatcagcctgagacccaacatctacacccatctat 285
QY 182 tttttcttccaatactatcaactcctgagatctgtttacacacatgtaagtcacacaa 241
DB 286 tttttcttccaatactatcaactcctgagatctgtttacacacatgtaagtcacacaa 345
QY 242 atgtctagtaattatgacacatcaggaagaatgaatcagttatcgtgtgtgtgagccag 301
DB 346 atgtctagtaattatgacacatcaggaagaatgaatcagttatcgtgtgtgtgagccag 405
QY 302 ctttctatcttgccttggtgaggtgacacgaatctctcctgagcgtacatgcttctt 361
DB 406 ctttctatcttgccttggtgaggtgacacgaatctctcctgagcgtacatgcttctt 465

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QY 362 gattgttttagtactatctgtcgccctccatcactcaagtatcatatgacacagactc 421
DB 466 gacaggttttagtactatctgtcgccctccatcactcaagtatcatatgacacagactc 525
QY 422 tgcctcaggtttagtactatctgtcgccctccatcactcaagtatcatatgacacagactc 481
DB 526 tgcctcaggtttagtactatctgtcgccctccatcactcaagtatcatatgacacagactc 585
QY 482 accctgactctcagcctgacacatctgtgacacccatgtatgatacacttctctcgaa 541
DB 586 attctactctccaggttgcacagctgtgacacccatgtatgatacacttctctcgaa 645
QY 542 gtccctgacatgctcagatctctgtgtgagacaacagcaatgagctgacatctc 601
DB 646 gtccctgacatgctcagatctctgtgtgagacaacagcaatgagctgacatctc 705
QY 602 ctgtgacgtgacatctcctatcaataccctgacacatctctctatatacacttctt 661
DB 706 ctgtgacgtgacatctcctatcaataccctgacacatctctctatatacacttctt 765
QY 662 atgtccgagcagatattgagatacagctgtgtaagtcgacaaaagaacatctggaga 721
DB 766 atgtccgagcagatattgagatacagctgtgtaagtcgacaaaagaacatctggaga 825
QY 722 tgtgttcccatcaattgtgtgtctctttttataglacagcgcgtctgtgtactctg 781
DB 826 tgtgttcccatcaattgtgtgtctctttttataglacagcgcgtctgtgtactctg 885
QY 782 caaccacacttcgcccagctcccaagacagaaagatgttctctctctatgtaac 841
DB 886 ctaccacacttcgcccagctcccaagacagaaagatgttctctctctatgtaac 945
QY 842 atgcacacatgctgaatcccttatatacacttggagacaagaggtlaaagagagc 901
DB 946 atgcacacatgctgaatcccttatatacacttggagacaagaggtlaaagagagc 1005
QY 902 tttaaaaggtgtgtgcaagatcttcttaalcaagaataa 943
DB 1006 tttaaaaggtgtgtgcaagatcttcttaalcaagaataa 1047

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RESULT 9
US-60-360-207-42178
; Sequence 42178, Application US/60360207
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
; FILE REFERENCE: CL001321
; CURRENT APPLICATION NUMBER: US/60/360, 207
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 47235
; LENGTH: 1071
; TYPE: DNA
; ORGANISM: HUMAN
US-60-360-207-42178

Query Match          63.9%; Score 602.2; DB 75; Length 1071;
Best Local Similarity 77.4%; Pred. No. 1.0e-170;
Matches 730; Conservative 0; Mismatches 213; Indels 0; Gaps 0;

QY 1 tatgaattggtaaatgacagacatcaatacagagttatctgtctggtttctcagatcga 60
DB 129 tatgaattggtaaatgacagacatcaatacagagttatctgtctggtttctcagatcga 188
QY 61 accttgctgaggtttccacccctgtgtgtcttcttgaattcttcaactgtgacatctt 120
DB 189 accttgctgaggtttccacccctgtgtgtcttcttgaattcttcaactgtgacatctt 248
QY 121 tggaaactgcacattatctagtgtaagcgtctggaacccaattatatacccccagta 180

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Db	249	tggaaataatgatgatcatcttctgtgtccggcctgtgattccaaatctccaaaccccatgta	308
Qy	181	ttttttcttaccaatcatcaactccctgtacttctgtgtaacccaatgttacaagttccca	240
Db	309	ctttttcttccaaataacttccctctgtcgtgacccgtgtgtcatccacaagaagtgctccaca	368
Qy	241	aatgtcagaataattatgagatcatcaagaagtaatacaattatcgtgtgtgtgtgaccca	300
Db	369	gattgtcatcaacaactctgagacacccgggaaggtgatacagctatgtgtgtgtgtgcca	428
Qy	301	gcttttcaatttcttgcgccttctgggggtactactgatacttcttcccttgcgcgtatgtcct	360
Db	429	gcttttcaatttcccttgcgccttctgtgtgttccacaagaatgcttcttgcgtgtgcatgtcct	488
Qy	361	tgtatgtgtttgaactatttgcctgtgcgcctccatcaactaactatgatactgacccaagact	420
Db	489	ttaacagttttgtagacatctgttgcgcctctccactactaagcatcatbtaaccaagaagtg	548
Qy	421	ctgcctcccaagtttggaacgtgcatactcctgggtttactgtgttttaactaagttgtgtgc	480
Db	549	ctgcctcccaagtttggaacgtgcatacttgtgtacagtggtgtcttcaagaacatccagttacaagtc	608
Qy	481	tacccttgactctccacgtctgcacactctgtgacccctatgtgataagatacaattctctgtga	540
Db	609	tacgtggaaccccttcagatgtgcacactgtgtgtgacacaagaagtggaaccattcttgcga	668
Qy	541	agtcctctgactctgtcccaagtatacttctgtgtgtgaagacaagaacaatgtgagctcgaactat	600
Db	669	agtcctctgtccctgtcccaagtttccctgtgtgtgatacgaagctaatgaagcagagctgtt	728
Qy	601	ccttctcagtgagcctcttccacataacacccctgacacatccatccctatatatgcttt	660
Db	729	ctctaataagtgctgttcttcttataaccgttaccctccatccctcatatcatatgcttt	788
Qy	661	tatttctcgaagcagatattgaaagatacaacagtctgcgaaggtcgacaaaagaacttggagac	720
Db	789	tatttctcgaagcagatattgaaagataagatacagactgaaggtctggcgaaagcatttggagac	848
Qy	721	atgtgtgtcccaactaaattgtgtgtgtctctttttatagtaagccgtrctcgttact	780
Db	849	atgtgtgtctcccaactcaactgtgtgtgtctcttcttcttctatgtgcactgtccatcatagttatct	908
Qy	781	gcaaacacacttgcgccaagcttccaaagaacccaagaagaagatcgtttctctcttcataatgaat	840
Db	909	gaagcacacatactccactacttccataagaagaccggggaaatggtgtctctcttttaatggat	968
Qy	841	catgtcacccaatgtcgaatccctctatatatacaacttgaagacaaggaagtaagaaag	900
Db	969	catcacacccaatgtcgaacccctcatcatcacacactcagaacccaagaagtaaggaagc	1028
Qy	901	ctttaaaggtgtgtgtgcaaggtcttcttaatacaagaataa	943
Db	1029	gttcaagaaggtgtgtgacaaagatcatatccctgtgttgaataata	1071

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RESULT 10
US-60-178-308-604/C
: Sequence 604: Application US/60178308
: GENERAL INFORMATION:
: APPLICANT: Bonazzi, Vivien
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEINS, AND USES THEREOF
: FILE REFERENCE: CLO00204
: CURRENT APPLICATION NUMBER: US/60/178, 308
: CURRENT FILING DATE: 2000-01-27
: NUMBER OF SEQ ID NOS: 3344
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 604
: LENGTH: 673
: TYPE: DNA
: ORGANISM: HUMAN
US-60-178-308-604

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Query Match	53.7%	Score	600.4	DB	56	Length	673
Best Local Similarity	99.8%	Pred	No. 4.5e-170				
Matches	601	Conservative	0	Mismatches	1	Indels	0
							Gaps
							0
QY	342	tccttgcgcgtcattgcttcctttgatttgatttgtagctatttgcgcctccattactcaag	401				
Db	673	TCCTGGCCGTCATGTCCTTTGATAGATTGTGAGCTATTGTGGGCTCTCCATTACTCAG	614				
QY	402	ttatcatgaccagagacctgcctcccaattggcagcgtgcattcccggttactgattta	461				
Db	613	TTATATATGACACGAGACTCTGCTCCATGGAATGGACGCTCATCCGgggTtactGgTTTA	554				
QY	462	gttaactcagttggtgtgtcattacacctgcacatcccaatgacactcgttgaacctta	521				
Db	553	GTAACTCAAGTGAGTTGTCTACCCGACTCTCCACCTGCCACTCTCTGACCCCTATGTGA	494				
QY	522	tagatcaactttctctgttgaagtcacctgcacgtctcaagtattccttgatttgagacaacag	581				
Db	493	TGAGTACACTTCTCTGTGAAGTCCCTGCATCTCTCAAGTTATCTTGTGTGAGACAACG	434				
QY	582	caaatgagagctgaactattcccttgcagtgagctctccatctaaataccctgcacactca	641				
Db	433	CAAAAGAGGCTTAACATTCTTCTGTGACAGGACCTCTCCATCTAATPACCCCGACACTCA	374				
QY	642	tccttatatcataatgcttttatttgcgcagacgatttgagataaagtctgctgaagtc	701				
Db	373	TCCCTATATACAAATCTTTTATTGTCGAGCAGTATGAGGTAAAGTCGTGGAAGGTC	314				
QY	702	gacaaaaacatttgggacatgtgtttcccaactaatgtgagtctctctttcttattagta	761				
Db	313	GACAAAAGCACTTGGGACATGTGGTCCCACTAATGTGTGTCCTTTTATTATGA	254				
QY	762	cagcgctctctgttgaactgtcaaccacttgcgccagctccaaggaaccaagaaagatgg	821				
Db	253	CAGCGCTCTCTGTGACCTGCAACCAACCTCTCCAGCTCCCAAGGACCAAGGAAAGATGG	194				
QY	822	ttctctctctcattggaatcatctgcacccatgctgaatcccttataatacaacttaga	881				
Db	193	TTTTCTCTCTCTAATGGAATCATTTGCACCCATCTCTGAATCCCTTATATATACACTTAGA	134				
QY	882	acaagaggtaaagaaaggctttaaaggcttggttgcaagatcttcttaalcaagaat	941				
Db	133	ACAAAGAGAGTAAGGAAGGCTTTAAAGGTTGGTTCGAAGACTCTTCTTAATCAAGAAAT	74				
QY	942	aa 943					
Db	73	AA 72					

```

RESULT 11
US-60-245-225-86/c
: Sequence 86, Application US/60245225
: GENERAL INFORMATION:
: APPLICANT: Beasley, Ellen
: TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
: TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
: TITLE OF INVENTION: PROTEINS, AND USES THEREOF
: FILE REFERENCE: CLO000885
: CURRENT APPLICATION NUMBER: US/60/245,225
: CURRENT FILING DATE: 2000-11-03
: NUMBER OF SEQ ID NOS: 705
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 86
: LENGTH: 46924
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(46924)
: OTHER INFORMATION: n = A,T,C or G
US-60-245-225-86

```

Query Match 56.6%; Score 534; DB 63; Length 46924;
Best Local Similarity 72.9%; Pred. No. 4.1e-149;
Matches 687; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 2 atgaattggtaaatgacgaacatcatatcagagatttattctgctgggttcttcagatcga 61
DB 45060 ATGAATTGGGAAAATGAGAGCTCCCAAAAAGATTATACTACTGCTCTCGAATAGG 45001
QY 62 ccttggctggagttccaccccttggctctcttgattcttcttaacatgagacatttt 121
DB 45000 GCTTGGCTGAATAATGCCCTTTTGTGTGCTCTGTTAATATCATACAAATCACCATTAT 44941
QY 122 ggaacatcgacattatcttctgagctgagcgcctgagacaaacttcaaccccatglat 181
DB 44940 GGAATATGTCTCATCATGATGATGCTGATTCGATCCCAACTTCATTAACCTCCATGAT 44881
QY 182 tttttcttccatctcatctacactctctgattcttctgttaacacacatgtacagttccaca 241
DB 44880 TTTCTTCTCACTAATCTCTCATCTTGTAGATCTCTGATACCACTACAGTCCCTCAT 44821
QY 242 atgtagtaaatattatcgacatcagaaagtaacagttatctgctgtgtatgagccag 301
DB 44820 ATGTTAGTAATATTGTTGTCACACAAAAGACATCACTATGCTGTGCTGTGTGCTGTG 44761
QY 302 ctcttcaatattctgagcttggggtgactgaatattctctctgagcgtatgctctt 361
DB 44760 CTGATCATCTCTCTGAGGCTAGGTTGTCACAGAGTGTCTCTGCTGTGCTGTATATGCTCT 44701
QY 362 gattggtttgagctatttctgagcctctcactatcactcaatgattacatgacagagactc 421
DB 44700 GACAGATATGTTGGCTGTTGTCAGACCCCTCCACTATGATGATCAATGAATATTGGTTC 44641
QY 422 tgcctccagttgagcagctgacatcctgagtttgaactgatttgaactgattgttctt 481
DB 44640 TGCTTAAGATGATGAGAGCTTCTCTATGAGCTATGTTGCGCACTGATGCTCATGCT 44581
QY 482 accctgactctcagctgacactctgtgacacctatgtatagatcaactctctctgtgaa 541
DB 44580 TCCCTTGACTTAACTAATGACACGCTGTGTCACAGAGAGGAGGACCTTTTCTGTGAG 44521
QY 542 gtcccttgcactgctcgaattatcttctgtgtgagacaaagaaatgtgagctgaactatc 601
DB 44520 GTGCTGCTCACTCTCAAGATTGTCATGTGTCACAAAAGCTTATTTGAGGCTGCTTC 44461
QY 602 ctgtcagtgagctctccatctcatatcccttgacactcatctatatacatatgctttt 661
DB 44460 TTCTTTAGTACTAATTTCTTAAATTCAGATGATGATGATGATGATGATGATGATG 44401
QY 662 atgtccgagcagatattgagagatacagctgtgagagtcgacaaagaaatgtgagaa 721
DB 44400 ATAGCTCAACAGATATTAAAAATCAGTGTGTCACAGAGAGGAGGCAAAAGCTTTGGGCA 44341
QY 722 tgttggttccatctcaattgtgtgtgtcttcttcttcttcttcttcttcttcttctt 781
DB 44340 TGTGTGTCACAGATGATGTCATGTCCTCTTATGTAAGAACGCACTTATATATATCT 44281
QY 782 caaacactctcgcagcagctcgaagacaaagaaagatgttctctctcttcttcttctt 841
DB 44280 CAACACTCTTCAATCCACTCTCAAGAGATGGGAAAGATGTTTCCCTCTTATGGAATC 44221
QY 842 atgtaccacatgtcgaatccccctatatatacatctaggaacaaagagatgaagaaagc 901
DB 44220 ATCAATATCATCTGTAAGTCTCCATCTACAGCTTATGAATTAAGATGAAGAGAGCC 44161
QY 902 tttaaaagttgtgtgagagagttcttcttcttcttcttcttcttcttcttcttcttct 943
DB 44160 TTCAAGAGGCTGATGTCACAGATCTTTTCTGTAAAGAAATTA 44119

; Sequence 27, Application US/60258250
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: C1001035-PROV
; CURRENT APPLICATION NUMBER: US/60/258,250
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 46924
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(46924)
; OTHER INFORMATION: n = A,T,C or G
US-60-258-250-27

Query Match 56.6%; Score 534; DB 64; Length 46924;
Best Local Similarity 72.9%; Pred. No. 4.1e-149;
Matches 687; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 2 atgaattggtaaatgacgaacatcatatcagagatttattctgctgggttcttcagatcga 61
DB 45060 ATGAATTGGGAAAATGAGAGCTCCCAAAAAGATTATACTACTGCTCTCGAATAGG 45001
QY 62 ccttggctggagttccaccccttggctctcttgattcttcttaacatgagacatttt 121
DB 45000 GCTTGGCTGAATAATGCCCTTTTGTGTGCTCTGTTAATATCATACAAATCACCATTAT 44941
QY 122 ggaacatcgacattatcttctgagctgagcgcctgagacaaacttcaaccccatglat 181
DB 44940 GGAATATGTCTCATCATGATGATGCTGATTCGATCCCAACTTCATTAACCTCCATGAT 44881
QY 182 tttttcttccatctcatctacactctctgattcttctgttaacacacatgtacagttccaca 241
DB 44880 TTTCTTCTCACTAATCTCTCATCTTGTAGATCTCTGATACCACTACAGTCCCTCAT 44821
QY 242 atgtagtaaatattatcgacatcagaaagtaacagttatctgctgtgtatgagccag 301
DB 44820 ATGTTAGTAATATTGTTGTCACACAAAAGACATCACTATGCTGTGCTGTATATGCTCT 44761
QY 302 ctcttcaatattctgagcttggggtgactgaatattctctctgagcgtatgctctt 361
DB 44760 CTGATCATCTCTCTGAGGCTAGGTTGTCACAGAGTGTCTCTGCTGTGCTGTATATGCTCT 44701
QY 362 gattggtttgagctatttctgagcctctcactatcactcaatgattacatgacagagactc 421
DB 44700 GACAGATATGTTGGCTGTTGTCAGACCCCTCCACTATGATGATCAATGAATATTGGTTC 44641
QY 422 tgcctccagttgagcagctgacatcctgagtttgaactgatttgaactgattgttctt 481
DB 44640 TGCTTAAGATGAGAGCTTCTCTATGAGCTATGTTGCGCACTGATGCTCATGCT 44581
QY 482 accctgactctcagctgacactctgtgacacctatgtatagatcaactctctctgtgaa 541
DB 44580 TCCCTTGACTTAACTAATGACACGCTGTGTCACAGAGAGGAGGACCTTTTCTGTGAG 44521
QY 542 gtcccttgcactgctcgaattatcttctgtgtgagacaaagaaatgtgagaaatgtgagaa 601
DB 44520 GTGCTGCTCACTCTCAAGATTGTCATGTGTCACAAAAGCTTATTTGAGGCTGCTTC 44461
QY 602 ctgtcagtgagctctccatctcatatcccttgacactcatctatatacatatgctttt 661
DB 44460 TTCTTTAGTACTAATTTCTTAAATTCAGATGATGATGATGATGATGATGATGATG 44401
QY 662 atgtccgagcagatattgagagatacagctgtgagagtcgacaaagaaatgtgagaa 721
DB 44400 ATAGCTCAACAGATATTAAAAATCAGTGTGTCACAGAGAGGAGGCAAAAGCTTTGGGCA 44341

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QY 722 tctgtcccaatcaatgtgtgtctcttttataagtaagcgcgtctgttacctg 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44340 TGTGGTCCACATGATGTGGTGTCCCTTTATGGAACAGCATTTATATGATCTT 44281
QY 782 caaccaccttcgcccagctcccaaggaagaagatgtttctctcttataatgaac 841
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44280 CAACCCACTTTCATCCACTTAAGGACTGGGGAAGATGGTTCCCTCTCTATGGAATC 44221
QY 842 atgcaccatgtcgaatcccttatataacttaggaagaagaagatgaagaagc 901
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44220 ATCAATCCATGTTGAACCTCCCTATCTACAGCCTTGAATAAATATGAAGAGGCC 44161
QY 902 tttaaaagtgtgtgaagaagcttcttaacaaagaataa 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 44160 TTCAAGAGGCTGATGCCAAGATCTTTTCTGTGAAGAAATTA 44119

RESULT 13
US-60-248-505-274/c
; Sequence 274, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 274
; LENGTH: 68686
; TYPE: DNA
; ORGANISM: human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(68686)
; OTHER INFORMATION: n = A,T,C or G
US-60-248-505-274

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Query Match 56.6%; Score 534; DB 63; Length 68686;
Best Local Similarity 72.9%; Pred. No. 4.9e-149;
Matches 687; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 2 atgaattggtaaatgacagcatatatacagaagttatctgcgcgggtttctcagatcga 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66687 ATGAATTGGGAATAATGAGAGCTCCCAAAAGAGTTTACTACTTGGCTTCTCAGATAGG 66628
QY 62 ccttgctggaagttccactcctgtgtctcttgaattcttactacactgtgacatctt 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66627 GCTTGGCTAACAAATGCCCTTTTGTGTGCTGTTAATATCATATACAAATCACCATAATT 66568
QY 122 ggcacatcgacatattatcagtgcaagcctggaacccaacttaaccccacatgtat 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66567 GGCATATGTCATCATGATGAGTGTGATCTGATCCCAAACTCATACCTCCATGTAT 66508
QY 182 ttttttttccaatcatatcactcctgacatcttgttataccaagaattacagttccacaa 241
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66507 TTCTTTTCTACTATCTCTCTCATCTTGTAGATCTCTGCTATACCAACATACAGTCCCTCAT 66448
QY 242 atgctagtaaatatlatgacacatcaagaagtaactagttatcgtgtgtctgtgacccag 301
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66447 ATGTGTGTAATAATATGTTGCAACAATAAGCCATCAAGTATGCTGTGCTGTGCTCCAC 66388
QY 302 ctttcaatctctgacctgtgggggactgaataatctctcctgagccatgtctctt 361
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66387 CTCATCATCTTCCCTGGCCCTAGGAGTACAGAGTCTCTCTTGGCTGTATATCTCTT 66328
QY 362 gattgtgttagctattgtgtgagcctctcatatcactcaagtatcatagaccagagctc 421
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66327 GACAGATATGTGCTGTTTGACAGACCCCTCCACTATGTAGTCAATCAATGAATTAATTGGTTC 66268

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QY 422 tgcctccagttgacagtcgacatccctgggttactgttttagtaactcagtggtgtct 481
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66267 TGCTTAAGGATGGAGCCTTCTCATGGCTCATTTGGTTTGGCAACTCAGTCTCGAGTCT 66208
QY 482 aacctgaactctcagctgcgacatctgtgacccctatgtatagatcaacttctctgtga 541
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66207 TCCCTTGTACTTAACATGCCCAGCTGTGTGCACCAAGGAAGTGACCACTTTTCTGTGAG 66148
QY 542 gtccctcactgcgtcaagttaatctgtgtgtgagaacaagaanaatggagctgaactatc 601
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66147 GTGCTGTCACTTTCAGAGTTTCTCATGTGCTGACACAAAGCCTATTGAGGCTGACCTTTC 66088
QY 602 ctgtcagtgagctcttccatctaatccccctgacacactcctatatacatatgtcttt 661
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66087 TTCTTATGTAGTAAATTTCTTCTAATTCAGATGACATGATCAATCTCTATGAGCTTC 66028
QY 662 atgtcagagcagatattgaagatcagttctgtgaagtgacaaaagaatltgggaca 721
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66027 ATAGCTCAAGCAGATTAATAAATCAGGTACAGCAAGAGACGCAAAAAGCATTTGGGACA 65968
QY 722 tctgtcccaatcaatgtgtgtctcttcttataagtaagcgcgtctgttacctg 781
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65967 TGTGGTCCACATGATTTGTGTGTCCCTTTTATGGAACAGCCATTTATATGATCTT 65908
QY 782 caaccaccttcgcccagctcccaaggaagaagatgtttctctcttataatgaac 841
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65907 CAACCCACTTTCATCCACTTAAAGGACTGGGGAAGATGGTTCCCTCTCTATGGAATC 65848
QY 842 atgcaccatgtcgaatcccttatataacttaggaagaagaagatgaagaagc 901
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65847 ATCAATCCATGTTGAACCTCCCTCATCTACAGCCTTGAATAAATATGAAGAGAGGCC 65788
QY 902 tttaaaagtgtgtgaagaagcttcttaacaaagaataa 943
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65787 TTCAAGAGGCTGATGCCAAGATCTTTTCTGTGAAGAAATTA 65746

```

```

RESULT 14
US-60-248-505-1606
; Sequence 1606, Application US/60248505
; GENERAL INFORMATION:
; APPLICANT: Beasley, Ellen
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; FILE REFERENCE: c1000918
; CURRENT APPLICATION NUMBER: US/60/248,505
; CURRENT FILING DATE: 2000-11-15
; NUMBER OF SEQ ID NOS: 1998
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1606
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: human
US-60-248-505-1606

```

```

Query Match 56.1%; Score 529.4; DB 63; Length 1510;
Best Local Similarity 72.7%; Pred. No. 1.9e-148;
Matches 683; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 2 atgaattggtaaatgacagcatatatacagaagttatctgcgcgggtttctcagatcga 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 atgaattgggaataatgagagcttcccaagaagttataactactgtgcttctcagatag 61
QY 62 ccttgctggaagttccactcctgtgtctcttgaattcttactacactgtgacatctt 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 gcttggtataaagtgcccctttgtgtgtcctgttaataatcaatacaatcaatcatt 121
QY 122 ggcacatcgacatattatcagtgcaagcctggaacccaacttaaccccacatgtat 181
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 ggcacatgttccatcatgaltggtgtgacttctgtatcccaaaacttaacccaatgtat 181

```

[illegible]

```

RESULT 15
US-60-162-248-93/c
: Sequence 93, Application US/60162248
: GENERAL INFORMATION:
: APPLICANT: Bonazzi, Valien
: TITLE OF INVENTION: ISOLATED HUMAN DRUG TARGET PROTEINS,
: TITLE OF INVENTION: NOCLETIC ACID MOLECULES ENCODING HUMAN DRUG TARGET PROTEINS
: TITLE OF INVENTION: AND USES THEREOF
: FILE REFERENCE: C1000123
: CURRENT APPLICATION NUMBER: US/60/162, 248
: CURRENT FILING DATE: 1999-10-29
: NUMBER OF SEQ ID NOS: 1476
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 93
:
: LENGTH: 642
:
: TYPE: DNA
: ORGANISM: Human
: US-60-162-248-93

```

Query Match	53.68;	Score 505.6;	DB 55;	length 642;
Best Local Similarity	99.28;	Pred. No. 2e-141;		
Matches 508;	Conservative 0;	Mismatches 4;	Indels 0;	Gaps 0;

OY	2	atgaattgggaaatgcgaagatcatcaacgaagattctctgcgggtttcttcagatcga	61
Db	514	ATGAATTTGGTAAATGACAGCATCATACAGAGATTATCTCGTGGGTTCTCAGATCGA	455
OY	62	ccttggtcgtagtlltccaactccttgtygtcttcttgatttcttcaactgtgaccacttt	121
Db	454	CCTTGGCGGGATTTCACATCTCTTGTTGGTCTTCTTGATTTCTTACACTGGACATCTTT	395
OY	122	ggcaatcgcgacattatctciagtgtcaagccttgagaccaactcaacttataccccaatgat	181
Db	334	GGCAATCTGACCATTAATTCTTAGTGTACAGCCTGAGACACCAACTCTCATACCCCATGTAT	335
OY	182	tttttcttacaactctatacactcctcgatccttltgttacaaccaatgltacagttccaaca	241
Db	334	TTTTTTCTTTACCAATCTCATACCTCTGGATCTTTGTTACACACATGTATACAGTCCCAAA	275
OY	242	atgcgtagaatattatcgcagatcaagaagaagtaaactgaattacgttgcgtgtgtagccag	301
Db	274	ATGCTAGTAAATTTATGACGACATGAGGAAGTATATCGATTCTGCGCTGTAGCCAG	215
OY	302	ctttcacaattctcgcgccttgagggtcctactgaatatcttctcgtgcgcgtcatgltcctt	361
Db	214	CTTTTCATATTTCTGGCCCTTGGGGGCTACTGAATATCTTCTCCGGCGGTCAATGTCCTTT	155
OY	362	gattggttltgaagctatttgcgcgcctctccatattacacagttatcagaaccaagagctc	421
Db	154	GATAGGTTTGAAGCTAATTTGTGGCCCTCTCCATTACAGTATCAATCAAGCACCAAGAGCTC	95
OY	422	tgacctcagatttgcgaagctgcatacctcgttgatttacttggttttgaactaagtgtygttct	481
Db	94	TGCCGTCAGTTGGCAGCTGCATCTGGGTTACTGGTTTATGATACTCAGTGTGTGCT	35
OY	482	accctgactctccagctgcgaactctgtgagacc	513
Db	34	ACCCGACTCTCCAGCTGCCACTCTGGACCCC	3

Search completed: August 25, 2002, 20:07:24
Job time: 6157 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 17:54:57 ; Search time 432.84 Seconds
(without alignments)
5945.102 Million cell updates/sec

Title: US-09-800-321A-3

Perfect score: 943

Sequence: 1 tatgaattggtaaatgaca.....tcttcttaataagaataa 943

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1737567 seqs, 1364410299 residues

Total number of hits satisfying chosen parameters: 3475134

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
1: /cgn2_6/ptodata/2/pna/US06_NEW.COMB.seq:*
2: /cgn2_6/ptodata/2/pna/US06_NEW.COMB.seq:*
3: /cgn2_6/ptodata/2/pna/US07_NEW.COMB.seq:*
4: /cgn2_6/ptodata/2/pna/US08_NEW.COMB.seq:*
5: /cgn2_6/ptodata/2/pna/US09_NEW.COMB.seq:*
6: /cgn2_6/ptodata/2/pna/US10_NEW.COMB.seq:*
7: /cgn2_6/ptodata/2/pna/US10_NEW.COMB.seq2:*
8: /cgn2_6/ptodata/2/pna/US60_NEW.COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	47.5	2940	7	US-10-027-632-111618
2	403.6	42.8	967	7	US-10-032-189-33
3	402	42.6	939	7	US-10-032-106-2
4	371.6	39.4	1014	5	US-09-965-422-9
5	371.6	39.4	1187	1	PCT-US02-03635-59
6	370	39.2	1007	5	US-09-965-422-7
7	370	39.2	1013	5	US-09-965-422-3
8	370	39.2	1014	5	US-09-965-422-5
9	370	39.2	1065	5	US-09-965-422-7
10	357	37.9	1005	5	US-09-965-422-11
11	357	37.9	1124	1	PCT-US02-03635-80
12	345	36.6	1035	5	US-09-546-986A-1
13	343.2	36.4	2197	1	PCT-US02-03635-96
14	319.6	33.9	1351	5	US-09-546-986A-5
15	318	33.7	971	5	US-09-981-566A-27
16	318	33.7	1162	1	PCT-US02-09923-112
17	309.4	32.8	942	5	US-09-907-218-9
18	309.4	32.8	1351	1	PCT-US02-09923-106
19	297.4	31.6	975	6	US-10-023-601-57
20	291.4	30.9	1411	5	US-09-546-986A-3
21	289.4	30.7	1188	6	US-10-210-782-1
22	289	30.6	961	6	US-10-023-601-59
23	275.6	29.2	1098	7	US-10-149-826-65
24	273	29.0	1026	1	PCT-US02-03635-82
25	270.2	28.7	987	6	US-10-023-601-29

26	265	28.1	806	7	US-10-027-632-29717	Sequence 29717, A
27	262	27.8	973	1	PCT-US02-09923-116	Sequence 116, App
28	255.8	27.1	963	6	US-10-025-806-55	Sequence 55, App1
29	255.6	27.1	945	6	US-10-098-754-21038	Sequence 21038, A
30	255.6	27.1	1301	1	PCT-US02-09923-91	Sequence 91, App1
31	254.4	27.0	1124	1	PCT-US02-09923-133	Sequence 133, App
32	253.4	26.9	938	5	US-09-965-422-35	Sequence 35, App
33	253.4	26.9	1701	1	PCT-US02-09923-114	Sequence 114, App
34	252.6	26.8	2053	1	PCT-US02-09923-83	Sequence 83, App1
35	251.6	26.7	948	5	US-09-965-422-23	Sequence 23, App1
36	250.6	26.6	941	6	US-10-023-601-75	Sequence 75, App1
37	250	26.5	948	5	US-09-965-422-19	Sequence 19, App1
38	248.8	26.4	966	6	US-10-025-806-109	Sequence 109, App
39	248.8	26.4	966	6	US-10-025-806-111	Sequence 111, App
40	248.4	26.3	949	5	US-09-965-422-21	Sequence 21, App1
41	248	26.3	1175	1	PCT-US02-01339-26	Sequence 26, App1
42	247.4	26.2	941	6	US-10-023-601-73	Sequence 73, App1
43	246.8	26.2	1023	6	US-10-023-601-37	Sequence 37, App1
44	246.6	26.2	971	6	US-10-023-601-79	Sequence 79, App1
45	245.8	26.1	1451	1	PCT-US02-03635-67	Sequence 67, App1

ALIGNMENTS

```
RESULT 1
US-10-027-632-111618
; Sequence 111618, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111618
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-111618
```

Query Match Best Local Similarity 47.5% Score 448; DB 7; Length 2940;

Matches 574; Conservative 0; Mismatches 210; Indels 0; Gaps 0;

QY	160	caaatcattacccccatgtatctttcttaccatcattcactctgtatcttcttga 219
DB	1	caaatcattacccccatgtatctttcttaccatcattcactctgtatcttga 60
QY	220	caccacatgtacagttccacaaatgtcagtaatttatgcagcatcggaaagtaac 279
DB	61	taccacacactacagttccatcattatgttgaataatgttgcacaaagacacatag 120
QY	280	ttaatcgtgcgtgttagccagcttccatattctcgtgccttgggggactaataatc 339
DB	121	ctatcgtgcgtgtgtgcccacccatcattcttctcgtgccttaggtgtcacaagagtgtc 180

```
QY 340 tctctgagcgcatactgctcttgaattgtgttgaagctattgtgcgcctccatactc 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 cctctgagctgtatgtctcttgacagatatgtgctgttggacagccctccactagt 240
QY 400 agtatcatgacacagagactctgcctccagatgtgcagctgcacccgggtactgttt 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 agtatcatgatatgtgtctctgctcctaagatgtgcagcctctccatggtcattgtt 300
QY 460 tagtaactcaatgtgtgtctctacccagctccagctccagctccagctccagctccatgt 519
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 cggcaactcagtgctgcagctctctctctgactcttaacatgacagcgtgtgtccaccaga 360
QY 520 gatagatcattctctgttgaagatccctgcacgtcctcaagttatctgttgttgacaaac 579
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 agtggaccactttctgtgtgagtggtgcctgcactctcaagttgcatgtgtgtgacacaa 420
QY 580 agcaaaagagctgaactattctctgtcagtgagctcttccatctaataccctgacact 639
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 gctcatgagctgagctctctctctttagtgaactaattctctcaatccagtgacatt 480
QY 640 catcctatacatatgcttattatgtccgagcagatattgaggaatacagctgtcgaag 699
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 gatcctcatctccatgctgctcagctcagctcagctcagctcagctcagctcagctcag 540
QY 700 tcgacaaaagcatttgggacatgtgttcccatctaattgtgtgtctctttttttag 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 acggcaaaaagcatttgggacatgtgtgtcccatcatgtgtgtgtccctcttttag 600
QY 760 tacagcgtctctgtgtacacgcaacacacacacacacacacacacacacacacacacac 819
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 aacgacattatattgattatcttccacacacacacacacacacacacacacacacacacac 660
QY 820 gttctctctctctatggaatcatgtgacacacacacacacacacacacacacacacacacac 879
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 661 gttctctctctctatggaatcatgtgacacacacacacacacacacacacacacacacacac 720
QY 880 gaacaagaggttaagaaaggtcttaaaagtgtgtgacaaagctctctctaatcaacaa 939
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 721 aaataaagatatgaagagccttcaagaggtgctgtccaaagaaactcttctcttaagaa 780
QY 940 ataa 943
    |||
Db 781 ataa 784
```

RESULT 2

US-10-032-189-33

Sequence 33, Application US/10032189

GENERAL INFORMATION:

```
APPLICANT: Alsobrook II, John P
APPLICANT: Tchernev, Velizar T
APPLICANT: Liu, Xiaohong
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Grose, William M
APPLICANT: Lepley, Denise M
APPLICANT: Burges, Catherine E
APPLICANT: Shinkets, Richard A
APPLICANT: Grose, William M
APPLICANT: Szekeres, Edward S
APPLICANT: Vernet, Corine A.M.
APPLICANT: Li, Li
APPLICANT: Casman, Stacie J
APPLICANT: Boldog, Ferenc L
APPLICANT: Gorman, Linda
APPLICANT: Gangoli, Bsha A
APPLICANT: Fernandes, Elma R
APPLICANT: Rieger, Daniel K
APPLICANT: Edinger, Shlomit R
APPLICANT: Gunther, Erik
APPLICANT: Millet, Isabelle
```

```
APPLICANT: Sciore, Paul
APPLICANT: Ellerman, Karen
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-228
CURRENT APPLICATION NUMBER: US/10/032,189
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,495
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/258,171
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 60/269,940
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/274,192
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: 60/277,826
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: 60/279,840
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/282,981
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/283,656
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/309,247
PRIOR FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: 60/311,754
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/313,331
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 260
SOFTWARE: Patentm Ver. 2.1
SEQ ID NO 33
LENGTH: 967
TYPE: DNA
ORGANISM: Homo sapiens
US-10-032-189-33
```

Query Match

42.8%; Score 403.6; DB 7; Length 967;

Best Local Similarity 65.1%; Pred. No. 1.7e-103;

Matches 595; Conservative 0; Mismatches 319; Indels 0; Gaps 0;

```
QY 2 atgaattggtaaatgacagcatcatcacaagagttattctgctgggtttctcagatcga 61
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 12 atgatatgaagaaatggaattcttctcactgatttccactcgggtttctcagacag 71
QY 62 ccttgctgaggttccacacctctgtgtctctctgatttcttctacactgacatcttt 121
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 cctcagctgagctcagctcctctctgtgtcttcttcttctctatctcattctgtctg 131
QY 122 gccaatctgacattatcttagtgcacgctctggacacaaactcatacccatgtat 181
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 132 gggaacaaacacatcatgtattatctcactgtgacccaactctcaacatccatgtat 191
QY 182 ttttcttaccatctcactcctctgattcttgttaacacaaatgtacagttccacaa 241
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 192 ttttcttcccaactcaacttcttctgattctgtttacacaaacggcatgttccacag 251
QY 242 atgctagtaattatgacacatcaggaagtaactagttatctgtgctgtgagccag 301
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 ctctgtgtaattctcagaggagacagacaataatccactatgtgtgtgtgtgtcag 311
QY 302 ctcttcatattctgctctgtgggctactagaaatctctctgctgctgcatgtcttt 361
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 ctgtaacatctctcagctgtggatctcaagaatgcttctcttaggaatgtatgtatc 371
QY 362 gatgtgtttagctattctgcgctctccatcattcagttatcagacacagagatc 421
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 372 gaccgtatgacgtgttgcagggccctccactcaactacagtagtcatgacacccctgt 431
QY 422 tgctcagttggagctgacatctgtgtgttactgtttagtaactagtggtgtct 481
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```


Db 432 tatgtcgtatggtcttactatcatggtcatgtgttttgcacactccatctgcaagc 491
QY 482 accctgactctcagctgcaactctgtgacccctatgtatgatactcttctgtgaa 541
Db 492 gtgtcactctgtctttaaactcttctgtgagaataatgagaactcttctgtgag 551
QY 542 gtccctgactctgcttaagtatacttctgtgtgagacaacagcaaatgagctgaacttc 601
Db 552 gtctccactctgtcgaagctgtgtgtgacactctatgtaactgtgaactcttc 611
QY 602 ctgttcactgtactctcactcactaataaccctgacactcactcactatcatacttc 661
Db 612 ttgttcactgtactatctctcttctgtacccgtgtgacataatctcactatagtcag 671
QY 662 attgtccagcaatgatgagatacagctctgtgaaagtcgcacaanaagcaatttggaca 721
Db 672 attgtcagcgagcagtcagagataaagtcagcaacagcgagcaagaagaattgttggaca 731
QY 722 ttgtgttccacttaattgtgtgtgtctctttttatagtaacgctctgtgtactcg 781
Db 732 tgtgtcccccacacacagtggttccctgtctacgacagctactatctgtctactcc 791
QY 782 caaccactctgcgcacagcaagcaagaatgtgtctctctctatcagatc 841
Db 792 cagcccgcaacaactctctcaggtacagggcaagtcactctctctctacacatc 851
QY 842 attgacccactgtctgaatcccttataatacacttagaacaagaagtaagaagc 901
Db 852 attacccactgtacacacccctacataatacactgaggaacaagatgtgaagaagca 911
QY 902 tttaaaagtggt 915
Db 912 cttaagaagtgct 925

RESULT 3
US-10-032-106-2
; Sequence 2, Application US/10032106
; GENERAL INFORMATION:
; APPLICANT: Peng, Zaoyuan
; APPLICANT: Yu, Zailin
; APPLICANT: Willey, Andrew
; APPLICANT: Hu, Qianjin
; TITLE OF INVENTION: METHODS FOR IDENTIFYING G-PROTEIN
; FILE OF INVENTION: COUPLED RECEPTORS ASSOCIATED WITH DISEASES
; FILE REFERENCE: 43311200700
; CURRENT APPLICATION NUMBER: US/10/032.106
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/258,070
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-032-106-2

Query Match 42.6% Score 402: DB 7: Length 939:
Best Local Similarity 65.0% Pred. No. 4.9e-103;

Matches 594: Conservative 0; Mismatches 320; Indels 0; Gaps 0;

QY 2 atgaattgtgtaaatgacagcatcacagagattatctcgtcgtgttctcagatcga 61
Db 1 atgatacagaanaaatggaagttcttctcactgattatccctacaggttctctcgaaag 60
QY 62 cctgtgctgagattccactccttctgtctctcttcttacttctacactgtgacatctt 121
Db 61 cctcagctgagcagctacgtctcttctgttcttcttcttacttactatctcacttctg 120
QY 122 ggcacatgcacatattctcagctgtcagcgtgacacaaacttatacccatgcat 181
Db 122 ggcacatgcacatattctcagctgtcagcgtgacacaaacttatacccatgcat 181

Db 121 gggacaacaaacatcatgttatctcacttggaacccacatcttcaactccatgtat 180
QY 182 ttcttcttccaaactatcatcactcttgatcttctgttacaacacatgttacaagtcacca 241
Db 181 ttcttcttccaaacctaagcttcttctgtgactgtgttacaacacagcatgttccacag 240
QY 242 atgtcagtaaatatcagcagcatcaggaagtaactcagttacgtgtgtgtgagccag 301
Db 241 ctctcgtttaaactccagggagcagacaatcaactccctatgtgtgtgtgtgtcag 300
QY 302 ctcttcaattctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 361
Db 301 ctgtacatctctcagcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 360
QY 362 gatgtgtttagactattctgcgcctcctcactatcactacagttacatcagcacaagaatc 421
Db 361 gaccgcatagagattgttggagccctccacatcacaagtagtcagacaccctgtctg 420
QY 422 tgccctcagtggtgagctgtcactcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 481
Db 421 tatgtgtgagtggtcttacttacttacttacttacttacttacttacttacttacttact 480
QY 482 accctgactctcgcgcgtcgcacactgtgacccctatgtatagatacacttctcgtgaa 541
Db 481 gtgtcactctgtctttaaactcttctgtgagaataataatagaacacttcttctgtgag 540
QY 542 gtccctgacactgtcgaattacttctgtgtgtgagaacaacagcaatgagctgaactatc 601
Db 541 gtctcactatgtcccaagctgtgctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
QY 602 ctgtcagtgagcctctcactatataccctgacactcactatcactatatacatagcttt 661
Db 601 ttgtcagtgactatctctctgttactcctgttcatatcaatcttctcactatagtcag 660
QY 662 attgcagcagcatgtatgagatacagctctgtgaagctgacaaagaacatctgtggaca 721
Db 661 attgcagcagcatgtatgagataaagttagcaacagggcagaagaattgttgggaca 720
QY 722 ttgtgtccactcactaatgtgtgtctcttcttcttatagtacagcgtctcgtgtactcg 781
Db 721 tgtgtcccccacacacagtggttctcctgttctacgacagcatatctatgtctactc 780
QY 782 caaccactctgcgcagctcccaagacaggaagaagatgttctctcttataagatc 841
Db 781 cagcccgcaacaactctcagatcagatcaggaagcaagtcactctctcttatacacatc 840
QY 842 attgacccactgtcgaatcccttataatacactttagaacaaggaagtaagaagc 901
Db 841 attacccactgtacacacccctcatalataatacactugagaacaggaatgtgaagaagca 900
QY 902 tttaaaagtggt 915
Db 901 cttaagaagtgct 914

RESULT 4
US-09-965-422-9
; Sequence 9, Application US/09965422
; GENERAL INFORMATION:

; APPLICANT: Casman, Stacie
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine
; APPLICANT: Spaderna, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Urial M

```

: APPLICANT: Taylor, Sarah
: APPLICANT: Gunther, Erik
: APPLICANT: Tcherenev, Velizar T
: TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 21401-132
: CURRENT APPLICATION NUMBER: US/09/965,422
: CURRENT FILING DATE: 2001-09-27
: PRIOR APPLICATION NUMBER: 60/236,286
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 60/236,284
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 60/237,581
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/238,735
: PRIOR FILING DATE: 2000-10-06
: PRIOR APPLICATION NUMBER: 60/240,736
: PRIOR FILING DATE: 2000-10-16
: PRIOR APPLICATION NUMBER: 60/260,019
: PRIOR FILING DATE: 2001-01-05
: PRIOR APPLICATION NUMBER: 60/260,338
: PRIOR FILING DATE: 2001-01-08
: PRIOR APPLICATION NUMBER: 60/262,156
: PRIOR FILING DATE: 2001-01-17
: PRIOR APPLICATION NUMBER: 60/262,498
: PRIOR FILING DATE: 2001-01-18
: PRIOR APPLICATION NUMBER: 60/263,133
: PRIOR FILING DATE: 2001-01-19
: PRIOR APPLICATION NUMBER: 60/263,691
: PRIOR FILING DATE: 2001-01-24
: PRIOR APPLICATION NUMBER: 60/266,109
: PRIOR FILING DATE: 2001-02-02
: PRIOR APPLICATION NUMBER: 60/271,634
: PRIOR FILING DATE: 2001-02-26
: NUMBER OF SEQ ID NOS: 127
: SOFTWARE: Patentia Ver. 2.1
: SEQ ID NO 9
: LENGTH: 1014
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-965-422-9

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Query Match      39.4%; Score 371.6; DB 5; Length 1014;
Best Local Similarity 62.5%; Pred. No. 1.0e-94;
Matches 581; Conservative 0; Mismatches 349; Indels 0; Gaps 0;

QY 14 aatgacagcatcatcagaggttatctctggtggttcagatcgacctggtgag 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 82 aatgagagcaacctcagaggttatctctggtggttcagatcgacctggtgag 141
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 ttccactcctgtgtctctctgattcttctacacgtgacacatcttggcaatcagc 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 142 aaggtctattgtgctcattgtattctgtatttacttaactatttggggaataccac 201
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 attatttagtgcagccctggacacaaattatataccccaagtatttttcttacc 193
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 202 atcatctgttctcgtcgtcgaaacccaagttcatactgcagatgttcttcttct 261
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 194 aatctacactcctggatcttctgttaccacacatgacagtcacgacacaaatgagta 253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 262 catctcctcctctgtcctcgtcttaccacgacagttatttcccgctcctgtgtaac 321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 254 ttatgcagcatcagaagaatcatcagttatcgtgctgtgtgacacatttataatt 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 322 ctgagggaacccaatgaacatactgcctatgtgtgtgtgtgttgcacttaactcc 381
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 314 ctggccttggggctactaatatctctcctcggcgatcagtgctcttgattgtgtgta 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 382 catgccttggtatcactggtgtgtcctcctcggctctgagtcgtctgtgacgcatgtg 441
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 374 gctatttggcgcctcctactactagttatcagtcagacagaacatgctcctcaattg 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 442 gctgtcgcgtcctcctcacttaccatgtcttaagtacatcacatcctgtgaccttg 501
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 434 gcaagtcacatcctgtgtactgttttagtaactcaatgtgtgtctacacctctc 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 502 gcatcatgtagtgcctcagtgagatagccacacccctgtgacagtcacacctcactc 561
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QY 494 cagctgcacactgtgacacctatgtatagataacttctctctgtgaagtcctgcactg 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 562 cagctgcctctgtgtggacatgcgcaagtgatatttcatctcgtgagtgctctgtctc 621
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 554 ctcaagttatctgtgttgagacacagcaaatgagctgacactcctctgtcagtgag 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 622 atcaagctgctgtgtgggacacacgttcaagagctgtgaccttltgtgtcagatc 681
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 614 ctcttcacatcaacccttgacacatcctatataatgtcttatttctgcagca 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 682 ctcttcttagtgcctgtctcatctatcctcgtctcctcctgtctatctgcacagca 741
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 674 gtatttgagatcagctgtctgtaagtcgacgaacaaacatttggagatgtgttccat 733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 742 gtttgagagatgaagtcagctacccggagagaagaacatctcgacctgtcttccac 801
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 734 ctatttggtgtctcttctttttagtacaagcgtctctgtgtacccgcaaccacttcg 793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 802 ctgacagtggtacacacatctttaggaacacatccttcaatgtatctgcagccagcaag 861
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 794 ccagctccaaagaccaaagaatgttctctctctatgtgaatcatgtcacacatg 853
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 862 agtagatccaggaagcaggaagttgtctctctctctacactgtgtacacgcagatg 921
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 854 ctgatacccttatatactacttaggaacaggaaggttaaggaagctttaaaggctg 913
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 922 cttaaccccttatttataccttgaagacgaaggttgaaaggtgaaaggtcaatgaag 981
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 914 gtgcagaagctcttcttaatcaagaataa 943
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 982 ctagcaaaagctcctggaggaataatttta 1011
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```

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RESULT 5
PCT-US02-03635-59
: Sequence 59, Application PC/TUS0203635
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: BAUGHN, Marian R.
: APPLICANT: TRIBOUTLEY, Catherine M.
: APPLICANT: NGUYEN, Damien B.
: APPLICANT: THORNTON, Michael
: APPLICANT: YAO, Monique G.
: APPLICANT: KALLICK, Deborah A.
: APPLICANT: GANDHI, Ameena R.
: APPLICANT: WALIA, Narinder K.
: APPLICANT: ARVIZU, Chandra
: APPLICANT: ELLIOTT, Vicki S.
: APPLICANT: HAFALIA, April J.A.
: APPLICANT: RAMKUMAR, Jayalaxmi
: APPLICANT: JIN, Pei
: APPLICANT: TANG, Y. Tom
: APPLICANT: YUE, Henry
: APPLICANT: REDDY, Roopa
: APPLICANT: BURFORD, Nell
: APPLICANT: LU, Dyung Aina M.
: APPLICANT: GRAUL, Richard C.
: APPLICANT: KAHN, Farrah A.
: APPLICANT: WALSH, Roderick T.
: APPLICANT: ISON, Craig H.
: APPLICANT: RICHARDSON, Thomas W.
: APPLICANT: GRIFFIN, Jennifer A.
: APPLICANT: WARREN, Bridget A.
: APPLICANT: YANG, Junning
: APPLICANT: LEE, Ernestine A.
: APPLICANT: HARLAND, Lee
: TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
: FILE REFERENCE: PI-0357 PCT

```


Query Match 39.2%; Score 370; DB 5; Length 1007;
Best Local Similarity 62.4%; Pred. No. 5.2e-94;
Matches 580; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

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QY 14 aatgacagcatcatcagaagttatctctcgtggttctccagatcgacttgcgtgag 73
DB 75 aatgagagcaacctagaaagtttcatctctttaggtttctctgattctcctcag 134
QY 74 ttccactctctgtgctctcttctgattcttctacactgtgaccactttggcaactgacc 133
DB 135 aaggttctatttggcccatatgattctgtattactactatttggggaataccacc 194
QY 134 attattctagtcacgcgtggaaccaaatctacatcccccagatatttttcttacc 193
DB 195 atcatctgttctcgtctcggaaccagcttcatatgcccagatatttctctcttc 254
QY 194 aatctacatctctgtgcttcttcttctacacatgtacagtcaccacaagttagta 253
DB 255 catctctctctctgtaacgcgtcttccacagaagtttattcccgctctctgttaac 314
QY 254 ttatcgacatcaggaagaatcagttatcgtgctgtgtagccagcttccatatt 313
DB 315 ctgttggaaccatgaanaactacgcctatggtgctgttctgttccacttaaac 374
QY 314 ctggccttggggctactcgaatatctctccctggcgatcgtctcttggattgta 373
DB 375 catgccttggaatccactgagtgctctcccgctctgattctcgtgacccgtatg 434
QY 374 gctatttgggcctctccacttactcagttatcatgacacagagactctccatg 433
DB 435 gctgctccgctctccctccctacacgtcttcttcatcactcactcgtgactg 494
QY 434 gcaagctcagctcgtggttactggtttagtaactcagtggtgtctaccctactc 493
DB 495 gcatctatgcatgagccatggaatagacacacccctgtgtacagttcacctacc 554
QY 494 cagctgcactcgtgacccctatgtagatcatcttctctgtggaactcgtgac 553
DB 555 cagctgcctctctgtggtgacatgcacagttgattcatctctgaggtccctgt 614
QY 554 ctcaagttatctgtgtgtggaacacagcaaaagagcttaactattcctgtgag 613
DB 615 atcaagctcgtcgtggtggaacacagtttcaacgagcgtgagcttctgtgag 674
QY 614 ctcttcatcattacaccccgacacatcactcattacatagatttattgtccag 673
DB 675 ctcttcttattagtcgtctcatcattcactcgtctccctgtgctacattgccc 734
QY 674 gtatttgagatcagctcgtggaagtcgacaacaaagcatttggagactgtg 733
DB 735 gtgttgagagattagtcagttacagagacagaagcattcgtgacctctctcc 794
QY 734 cttaattgtgtgtctcttcttctttagtaacgcgtctctgttaccctgacac 793
DB 795 ctgacagttgttccacacttctttagaaccatcattcttctgacgcagcc 854
QY 794 cccagctcccaaggaacgaagatggttctctcttcataggaactgaccacat 853
DB 855 agtgcagatccagggacccgggcaagtgttctctctcttcttcaactgtgaac 914
QY 854 ctgaatccctatataatacacttagaacaagaaggttaagaagccttaagaag 913
DB 915 cttaaccctctatttatacacttgaagatcaagaaggtgaaagggatctaa 974
QY 914 gtgcgaaggtctcttctaatcaagaataa 943
DB 975 ctgcaagaagctctggaagtaaatattta 1004
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RESULT 7
US-09-965-422-3
; Sequence 3, Application US/09965422

```
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Casman, Stacie
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine
; APPLICANT: Spaderma, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Li, Li
; APPLICANT: Malvanekar, Urial M
; APPLICANT: Taylor, Sarah
; APPLICANT: Gunther, Erik
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO: 3
; LENGTH: 1013
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-965-422-3

Query Match 39.2%; Score 370; DB 5; Length 1013;
Best Local Similarity 62.4%; Pred. No. 5.2e-94;
Matches 580; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

QY 14 aatgacagcatcatcagaagttatctctcgtggttctccagatcgacttgcgtgag 73
DB 81 aatgagagcaacctagaaagtttcatctctttaggtttctctgattctcctcag 140
QY 74 ttccactctctgtgctctcttctgattcttctacactgtgaccactttggcaactgacc 133
DB 141 aaggttctatttggcccatatgattctgtattactactatttggggaataccacc 200
QY 134 attattctagtcacgcgtggaaccaaatctacatcccccagatatttttcttacc 193
DB 201 atcatctgttctcgtctcggaaccacagcccatatgcccagatgtatttctctcttc 260
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[illegible]

```

RESULT      8
US-09-965-422-5
: Sequence 5' Application US/099654222
:
: GENERAL INFORMATION:
:
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Gasmán, Stacie
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Dickson, Kevin
: APPLICANT: Vernet, Corine
: APPLICANT: Spaderna, Steven K
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Gerlich, Valerie
: APPLICANT: Ellerman, Karen
: APPLICANT: Edinger, Shlomit
: APPLICANT: MacDougall, John R
: APPLICANT: smultison, Glenda
: APPLICANT: Li, Li
: APPLICANT: Malyankar, Urial M
: APPLICANT: Taylor, Sarah
: APPLICANT: Gunther, Erik

```

```

? APPLICANT: Tchernev, Velizar T
? TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
? FILE REFERENCE: 21401-132
? CURRENT APPLICATION NUMBER: US/09/965,422
? CURRENT FILING DATE: 2001-09-27
? PRIOR APPLICATION NUMBER: 60/236,286
? PRIOR FILING DATE: 2000-09-28
? PRIOR APPLICATION NUMBER: 60/236,284
? PRIOR FILING DATE: 2000-09-28
? PRIOR APPLICATION NUMBER: 60/237,581
? PRIOR FILING DATE: 2000-10-03
? PRIOR APPLICATION NUMBER: 60/238,735
? PRIOR FILING DATE: 2000-10-06
? PRIOR APPLICATION NUMBER: 60/240,736
? PRIOR FILING DATE: 2000-10-16
? PRIOR APPLICATION NUMBER: 60/260,019
? PRIOR FILING DATE: 2001-01-05
? PRIOR APPLICATION NUMBER: 60/260,338
? PRIOR FILING DATE: 2001-01-08
? PRIOR APPLICATION NUMBER: 60/262,156
? PRIOR FILING DATE: 2001-01-17
? PRIOR APPLICATION NUMBER: 60/262,498
? PRIOR FILING DATE: 2001-01-18
? PRIOR APPLICATION NUMBER: 60/263,133
? PRIOR FILING DATE: 2001-01-19
? PRIOR APPLICATION NUMBER: 60/263,691
? PRIOR FILING DATE: 2001-01-24
? PRIOR APPLICATION NUMBER: 60/266,109
? PRIOR FILING DATE: 2001-02-02
? PRIOR APPLICATION NUMBER: 60/271,634
? PRIOR FILING DATE: 2001-02-26
? NUMBER OF SEQ ID NOS: 127
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 5
? LENGTH: 1014
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-09-965-422-5

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Query Match	39.2%	Score 370	DB 5	Length 1014
Best Local Similarity	62.4%	Fred. No. 5.2e-94		
Matches 580	Conservative	0	Mismatches 350	Indels 0
				Gaps 0
QY 14	aatgcagcatcatacaagaattattctgcgagggtttctcagatcagcactgctgctggag	73		
DB 82	aatggagcaacacttagcaggtttcatctctttagggttttcgtatctcagttac	141		
QY 74	tttccactcttggtgtcttcttcttgattcttcaacactgtagacactcttggacaatctgac	133		
DB 142	aaggtctctattgttgcatatctgattcttgatttcttaacactatttggagatatccac	201		
QY 134	attattcttagtctcagcgcctggacacccaactctaccccaatgattttttttacc	193		
DB 202	atcatcttcggtttccgcctggaaacccaagctctatagcgaatatttctcttctt	261		
QY 194	aatctatcactctcgtgattcttgtttacacacatgataagttccacaatgctagaaat	253		
DB 262	catctctctctctcttaccgcgtcttccacagcagtgattatctccacagctcctgttaac	321		
QY 254	ttatgcagcatcaggaagaagtaactgaattatgttggtctgttagccagctttcatatt	313		
DB 322	ctgttggaacccaatgaanaactatgcgcatagtgtgctgtttgtttcaaccttaacaatcc	381		
QY 314	ctgscgttggtggagctcagaaatattcttcgcgscgtcatcttccttgattgtgttga	373		
DB 382	catgcctcgttgatccacatcagtagtgcctctcccgctctcagatgttctgtgacccgtatgt	441		
QY 374	gctatttctgcgcctctccatattccagttatcagaacacagagactctgctccagttg	433		
DB 442	gtgtctgcgcgtctccctccatctaacctgtcttaatgacatccatccatctgtacgtgctg	501		
QY 434	gcagctgaatccctggttactggtttttagaactcaatgattgttttctaacctgacttc	493		

Db 502 gcaactatgacatggtctagtcagatgacccaccocctgacagctccaccctcaacctg 561
QY 494 cagctgcacacctctgtaacccctatgtaatacaattctctgtaagctccctgaac 553
Db 562 cagctgcacacctctgtaacccctatgtaatacaattctctgtaagctccctgaac 621
QY 554 ctcaagatattctgtgtgagacacagcaaatgagctgaactatctctgtcaagtgag 613
Db 622 atcaagctggtctgtgtgagacacagcaaatgagctgaactatctctgtcaagtgag 681
QY 614 ctcttcacatcaataacccctgacacatcctctatataatgctcttattgtccgagca 673
Db 682 ctcttcacatcaataacccctgacacatcctctatataatgctcttattgtccgagca 741
QY 674 gtattgagatcacagctctgctgaaggtcgaacaaagacattgtagacatgtgtcccat 733
Db 742 gtgttgagatcacagctctgctgaaggtcgaacaaagacattgtagacatgtgtcccat 801
QY 734 ctattgtgtgtctctctttttatagtaacagcgtctgtgtacatcctgcaacacacatcg 793
Db 802 ctgacagctgacacacatcttattatggaacacacatcctctatctgtcagcagcaag 861
QY 794 cccagctcccaaggaagcaagaaatggtctctctctctctctatgtaacatctgacacacatg 853
Db 862 agtagatccaggaagcaagaaatggtctctctctctctctctctctctctctctctctctct 921
QY 854 ctgaatcccttatatactactaggaacaggaaggaaggaaggttttaaaagtgtg 913
Db 922 cttaacaccttatattatacctctgagatcaagaaggtgtaaaagggcatataaagaagt 981
QY 914 gtgcagaagctctcttaatacaagaataa 943
Db 982 ctgacaaagctctggaagtaataatttta 1011

RESULT 9
US-09-546-986A-7
: Sequence 7, Application US/09546986A
: GENERAL INFORMATION:
: APPLICANT: Powers, Scott
: APPLICANT: Yang, Jianxin
: APPLICANT: Cutler, Gene
: APPLICANT: Tularik Inc.
: TITLE OF INVENTION: Novel G-Protein Coupled Receptors
: FILE REFERENCE: 018781-004720US
: CURRENT APPLICATION NUMBER: US/09/546,986A
: PRIOR FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 09/524,730
: NUMBER OF SEQ ID NOS: 16
: SOFTWARE: Patentln Ver. 2.1
: SEQ ID NO 7
: LENGTH: 1065
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (26)..(1030)
: OTHER INFORMATION: human breast cancer amplified G-protein coupled
: OTHER INFORMATION: receptor 4 (BCA-GPCR-4)
US-09-546-986A-7

Query Match 39.2%; Score 370; DB 5; Length 1065;
Best Local Similarity 62.4%; Pred. No. 5.3e-94;
Matches 580; Conservative 0; Mismatches 350; Indels 0; Gaps 0;

QY 14 aatgacagcatcatacaggaattatctctgctggttcacagatcgacctgtgag 73
Db 98 aatgagagcaaccagaggtttcatccttttaggtttctgttatgtcagttacag 157
QY 74 ttccacctctgtgtctctctgtattcttaacatgtgacacatcttgcaatctgacc 133

Db 158 aaggtctattctgtctatattatctgtatttacttaactatttctggtgaataaccac 217
QY 134 attattagtgtaacgctctggaacccaacttaacttaacccatgtattttcttacc 193
Db 218 atcaatctgtttctctgtctggaacccaacttaacttaacccatgtattttcttacc 277
QY 194 aatcatcactctggaatcttctgttacacacatgtacagtcacccaatgtctgtaaat 253
Db 278 catctctctctctgtacacgctgtcttaacagagtgatttctccacgctctgtgtaac 337
QY 254 ttatgacatcacgaagaatatacagttatctgtgtgtgtgtgagccagctttcataatt 313
Db 338 ctgtggaacacacgaataactatcgcctatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 397
QY 314 ctgacgttggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 373
Db 398 catgacctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 457
QY 374 gctattgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 433
Db 458 gtgtgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 517
QY 434 gcaatctgacatctgt 493
Db 518 gcaatctgacatctgt 577
QY 494 cagctgcacacctctgtaacccctatgtagatgaatctctctgtgtaagctcccgacgt 553
Db 578 cagctgcacacctctgtaacccctatgtagatgaatctctctgtgtaagctcccgacgt 637
QY 554 ctcaagttatctgtgtgagacacagcaaatgagctgaacattctctctgtctgtcagtgag 613
Db 638 atcaagctggtgtgtgtgagacacagctttaaagagctgtgtgtgtgtgtgtgtgtgtgtgt 697
QY 614 ctcttcacatcaatccctgacacatccttatatcatatgctttattgttccgagca 673
Db 698 ctcttcacatcaatccctgacacatccttatatcatatgctttattgttccgagca 757
QY 674 gtattgagatcacagctctgctgaaggtcgaacaaagacattgtagacatgtgtgtcccat 733
Db 758 gtgttgagatcacagctctgctgaaggtcgaacaaagacattgtagacatgtgtgtcccat 817
QY 734 ctattgtgtgtctctctttttatagtaacagcgtctgtgtacatcctgtaacacacatctg 793
Db 818 ctgacagtggtgacacatcttattatggaacacacatccttatctgtatctgacagcagcaag 877
QY 794 cccagctcccaaggaagcaagaaatggttctctctctctctctctctctctctctctctctct 853
Db 878 agtagatccaggaagcaagaaatggttctctctctctctctctctctctctctctctctctct 937
QY 854 ctgaatcccttatatactactaggaacaggaaggaaggaaggttttaaaagtgtg 913
Db 938 cttaacaccttatattatacctctgagatcaagaaggtgtaaaagggcatataaagaagt 997
QY 914 gtgcagaagctctcttaatacaagaataa 943
Db 998 ctgacaaagctctggaagtaataatttta 1027

RESULT 10
US-09-965-422-11
: Sequence 11, Application US/09965422
: GENERAL INFORMATION:
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Casman, Stacie
: APPLICANT: Padigaru, Muralidhara
: APPLICANT: Dickson, Kevin
: APPLICANT: Vernet, Corine
: APPLICANT: Spaderna, Steven K
: APPLICANT: Shenoy, Suresh G
: APPLICANT: Gerlach, Valerie
: APPLICANT: Ellerman, Karen

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; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenna
; APPLICANT: Li, Li
; APPLICANT: Malanker, Uriel M
; APPLICANT: Taylor, Sarah
; APPLICANT: Gunther, Erik
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 11
; LENGTH: 1005
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-965-422-11

Query Match      37.9%; Score 357; DB 5; Length 1005;
Best Local Similarity 61.4%; Pred. No. 2.4e-90;
Matches 573; Conservative 0; Mismatches 360; Indels 0; Gaps 0;

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Db 355 cttatattctctgcaactggctcccaatgaatgatctcttgctgctacatgacctg 414
Qy 362 gattggtttgtagctattgtgcgcctccatctacatgctatcatgacacagagac 421
Db 415 gatcggtaactgtgtctgcaaacccctccactatgtatgtaactcaatgaacacagct 474
Qy 422 tgcctcagttgcaagctgcatccttggttactggttttagtaactcagtggtgtct 481
Db 475 tgcacaagctgcatctatctcttgctcagtggtttgcttgcttccatcatcagac 534
Qy 482 accctgactcagctgcaactcgtgaaccctatgtatgatatgaacttctctgtga 541
Db 535 accttaacttgcaattgctctcctgtggaacacatagctgtaacatttatctgaa 554
Qy 542 gtccctgcaactgctcaagttatcttggttgaacaacagcaaatgaagctgacatc 601
Db 595 gtacacagctctctcaagttgctgtgtggaacacacgttcaatgtatgtgctttt 654
Qy 602 ctgtgaatgagctctccatcaataccctgaacatcctctatataatgtcttt 661
Db 655 gtgttagtgtctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 714
Qy 662 atgtccagcagctatgtgaagacagctgtgtgaaggtgcacaagaagattgggaca 721
Db 715 ataccacagctgtgtgtgaagacacatcagtagaggaagacataaagctccagacc 774
Qy 722 tgtgttcccatctaatgtgtgtctctttttagtaagaacgctctctgtgtacctg 781
Db 775 tgtctctccacacttaagtggtgatatactctatgacacataatctactgtacctg 834
Qy 782 caaccaccttgcgcacgctcccaaggaacgaagaatgtttctctctctatgaatc 841
Db 835 caactagtgacagctatgcccaggaacgaagatttctccctctctacacatg 894
Qy 842 atggacccatgtctgaatcccttatataatacttaggaacgaaggaaggaagc 901
Db 895 gtacccccacttaaatctcatcatcatttaaggaacgaagataagaagagct 954
Qy 902 tttaaaagtgtgtgtgaagatctcttcaatc 934
Db 955 ctgaggaactctctcgggaataattgtgtctc 987

RESULT 11
PCT-US02-03635-80
; Sequence 80, Application PC/TUS0203635
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: THORNTON, Michael
; APPLICANT: YAO, Monique G.
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Nairinder K.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: JIN, Pei
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: REDDY, Roopa
; APPLICANT: BURFORD, Neil
; APPLICANT: LU, Dung Anna M.
; APPLICANT: GRAUL, Richard C.
; APPLICANT: KAHN, Farrah A.
; APPLICANT: WALSH, Roderick T.
; APPLICANT: ISON, Craig H.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.

```

APPLICANT: YANG, Junming
APPLICANT: LEE, Ernesline A.
APPLICANT: HARLAND, Lee
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0357 PCT
CURRENT APPLICATION NUMBER: PCT/US02/03635
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/267,322; 60/271,215; 60/274,551; 60/278,507;
60/280,597; 60/281,107; 60/282,121
PRIOR FILING DATE: 2001-02-07; 2001-02-23; 2001-03-08; 2001-03-23;
2001-03-30; 2001-04-02; 2001-04-06
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PERL Program
SEQ ID NO 80
LENGTH: 1124
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7477359CB1
PCT-US02-03635-80

Query Match 37.9%; Score 357; DB 1; Length 1124;

Best Local Similarity 61.4%; Pred. No. 2,5e-90;

Matches 573; Conservative 0; Mismatches 360; Indels 0; Gaps 0;

QY 2 ataattggtggaatgacagacatcacagaggttatctctgtgtgttcctgagatcga 61
DB 101 atggagattgggcaatgagagttcccaatgagattccctcttaagctcttaagacac 160
QY 62 ccttggtcgtgagttccacccctgtgtctctcttgaattcttacaactgtgacacatt 121
DB 161 cctgcgtcgtgaggtctgtctcttcttattgttcttcttcttcttccctgaccctgtg 220
QY 122 ggaactcgtacattatcttaagtgtaacgctgtgacacaaattatatacccaatgat 161
DB 221 ggaactcgtacattatcttaagtgtaacgctgtgacacaaattatatacccaatgat 280
QY 182 tttcttccacatcatcatcctcgtgacattgtttacacacatgtagtcacacaa 241
DB 281 tttcttccacacactctcttcttaactggaactgtcttcttcttcttcttcttctcctcag 340
QY 242 atgctgtaataattatgacagcatcaggaagtaacagttatcgtgtgtgtgagccag 301
DB 341 accctagttacttgaacagacaaagacagcatcacttaagctgtgtgtgtgtgtgtgtg 400
QY 302 ctttcatatttctggtcgt 361
DB 401 cttcatattctctcgtgacactggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 460
QY 362 gattgtttgttagctatttctggtcgtctctcatcttactcaagttactgacacagaaactc 421
DB 461 gatcgtgtacattgtctgtcgtcaaacctctcactatgtatgtatcatgtaacccaagcttc 520
QY 422 tgcctcgaattgtgacatgcatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 481
DB 521 tgcacacacgtgtgacatctctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 580
QY 482 accctacatctcagctgacacactgtgacacctatgtgtgtgtgtgtgtgtgtgtgtgtgt 541
DB 581 accttacttgaatgt 640
QY 542 gtccctgacatgctcaagtatctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 601
DB 641 gtacagcctctctcaagt 700
QY 602 ctgtcgaatgt 661
DB 701 gt 760
QY 662 atgtgtcgtgaggt 721

DB 761 ataactcaagctgt 820
QY 722 tgt 781
DB 821 tgtctctccacacttaagtggt 880
QY 782 caaccacacttgcgcacgtcctcgaacccaaggaagatgtgtgtgtgtgtgtgtgtgtgtgt 841
DB 881 caaccatgtgacgtatgtgcacaggaacgaaggttatctctcctcttcaacacatg 940
QY 842 atgcacacatgt 901
DB 941 gtgacccccaacttaactatctatctatctatctatctatctatctatctatctatctatct 1000
QY 902 tttaaaagt 934
DB 1001 ctgaggaactctctcgtggaataatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1033

RESULT 12

US-09-546-986A-1

Sequence 1, Application US/09546986A

GENERAL INFORMATION:

APPLICANT: Powers, Scott

APPLICANT: Yang, Jianxin

APPLICANT: Cutler, Gene

APPLICANT: Tularik Inc.

TITLE OF INVENTION: Novel G-Protein Coupled Receptors

FILE REFERENCE: 018781-004720US

CURRENT APPLICATION NUMBER: US/09/546,986A

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 09/524,730

PRIOR FILING DATE: 2000-03-14

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1

LENGTH: 1035

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (42)..(974)

OTHER INFORMATION: human breast cancer amplified G-protein coupled

OTHER INFORMATION: receptor 1 (BCA-GPCR-1)

US-09-546-986A-1

Query Match 36.6%; Score 345; DB 5; Length 1035;

Best Local Similarity 61.5%; Pred. No. 5.8e-87;

Matches 352; Conservative 0; Mismatches 345; Indels 0; Gaps 0;

QY 30 aagagttatctcgtcgt 89
DB 61 aagccttcaactcctctcgt 120
QY 90 tctcttctgtatcttcaactgt 149
DB 121 tctcttctgt 180
QY 150 gcttggaacacaaacttcaaccccatgtatcttcttcaacatctcaactcctcgtg 209
DB 181 ggtgtgatctcaactcacaagcccatgtatcttcttcaactcctcctcgtgtgtgtgtgtgt 240
QY 210 atcttgttacaacacatgtacagtcacacaaatgtctgtgtgtgtgtgtgtgtgtgtgtgtgt 269
DB 241 acctcgttacaacacacagacagtcacctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
QY 270 aagtaatacgtatcgt 329
DB 301 aagcctcagatgt 360
QY 330 ctgaatactctcctcgt 389


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Db 361 cggagtgatcgtctctgcccgcattgacctgacccgtacgtgcccagctgcaagccc 420
Qy 390 tccattactacgtatcatgacacagacctgctccagcttggaagctgcaagctcgtg 449
Db 421 tgcattatccgtctcattcattgacagctgctctgtaagcagcgtgctgctgagc 480
Qy 450 ttactggttttaactacgtggtgtgtgtctacccctgacatccagctccagctcgtg 509
Db 481 tcagtggtctcgcaactcctctgcaagtggtcccgagtgcaatgcaatccctcgtg 540
Qy 510 accctatgtatagatcattctctgtgtaagtcctcgacagctcgaatctctgtg 569
Db 541 ggcggcagggcgacgaacactttctgtgagtgccggcgagtgatcaagctgctg 600
Qy 570 ttgagcaacagcaaatgagtgtaactctctgtcagtgagctctccatcaat 629
Db 601 ctgacacgcgtatgaaatgacacacactgctgtgctggtgacctctctgtgtg 660
Qy 630 cctggaactacatcatatcatgcttttattgtgcccagagatattgagatacag 689
Db 661 cctggtctcctacatcctctctcctatggtcttattgcccggagtgatccag 720
Qy 690 ctgctgaagtcgcaaaaagcatitggagcatgtgtcccatcaattgtgtgtc 749
Db 721 ccccaagggagcacaagaagccttggagcgtgtccctccacgtatgatgtctcc 780
Qy 750 ttttatagtacagcgtctctgtgtacgtcaacacacctgcccagctcaagaagc 809
Db 781 tctctaccacactgattatcatgtatctgacgccccctccagctactccaaagc 840
Qy 810 aaggaagatggttctctctctatgaaatcttgaccacatgctgaatccctatat 869
Db 841 agggcaaatctatctctctctatccataacacccacactctcaatccctcct 900
Qy 870 atcactatggaagaggaagtaaggaagcttaaaagtgtgtgcaagatct 926
Db 901 acacccctggaataaagatagaagggtctgtgaggaactctgtgccaagatct 957

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; FILE REFERENCE: PI-0357 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/03635
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/267,322; 60/271,215; 60/274,551; 60/278,507;
; 60/280,597; 60/281,107; 60/282,121
; PRIOR FILING DATE: 2001-02-07; 2001-02-23; 2001-03-08; 2001-03-23;
; 2001-03-30; 2001-04-02; 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 96
; LENGTH: 2197
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 55019501CB1
PCT-US02-03635-96

Query Match 36.48; Score 343.2; DB 1; Length 2197;
Best Local Similarly 61.3%; Pred. No. 2,3e-86;
Matches 552; Conservative 0; Mismatches 348; Indels 0; Gaps 0;

Qy 22 catcataggaagtaattctctgctgggtttctcagatccagctggtgagttccact 81
Db 288 caaccacaaggaacttattcctctcgtgacatctccgaagagcatggtgagctccag 347
Qy 82 cctgtgtctctctgtatcttctacactgtgacatctcttgcaatctgacatctatct 141
Db 348 ctgtgacgtctcctctgtgtgtctacatcttgcgtatgctggtggaacatctctacatc 407
Qy 142 agtgcagcctgagacaacaaacttcaatcccatgtatcttttcttacaatctatc 201
Db 408 ggtatcccaatggtatcctcagctcacaagcccatgtatcatatctctcagccactgt 467
Qy 202 acctctgactctgtgtacacacacatgtacagctcccaaatgtagtaattatgag 261
Db 468 ctctctgactctctgtacacacacacacacacacacacacacacacacacacacac 527
Qy 262 catcaagaagtaactgactgctgtgtgtgagccagcttttcatattctgacct 321
Db 528 ctccagaagaacatcatgactgagtgctgcaagtgcaatgagccatcttccactgct 587
Qy 322 gggggtactgaaatattctctctgcccgtcaatgctcttgatgtgttgatctat 381
Db 588 ggggtgacagagtgctgtctctgtgcccagatgctctgacgcgtacagctgacatct 647
Qy 382 tcggcctctcatattcactgattatcatgacacagaagctcgtccctcagttgagctgc 441
Db 648 tgaagcaactccgcatgctatcatcatgacacgcgcacactcgcagagctcgtgctat 707
Qy 442 atcctggttactgtgttttgaactcagtggtgtgttctacactgactctcagctg 501
Db 708 ggcctggtcagcgtctggaactcctcctgttcaagtgatcctcgtgacagagcaattgc 767
Qy 502 actctgtgacccctatgtatgatactcaacttctgtgaaagctccctgcaatgct 561
Db 768 ttctgtgcccaggtgtgtgcaacactctctctgtgaggtgccaagcatgataagct 827
Qy 562 atctgtgttgagcaacagcaaatgagctggaactatctctgtgaagtgccttcca 621
Db 828 gtccgtgctgatactacgacggaatgacacccctgctgctgctgctgctccttct 887
Qy 622 tctaatccctgacactcctcatatcatatgacttttattgtccgagcagatgag 681
Db 888 gctgtcctcctctgcccctcatcctcctcctcctcctcctcctcctcctcctcctc 947
Qy 682 gatacagctcgtcgaagtgacaaaagcaatgtggagcatgtgttccatcaattgt 741
Db 948 gatcagctcctccagggagcagcaagccttggagactgtgtcttccacactgtgt 1007
Qy 742 ggtgtccttttatagtacagcgtctgtgttacttgcaacactctcgcacactc 801

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Db 1008 gttctccctctcttacctgcccgcacattacatgtaacctgcaagccgacatccagttatc 1067
Qy 802 caaggaccagaagaatggtttctctctctctatgaaatattgcaaccatctcgaatcc 861
Db 1068 aacggagacaggaagatctatctccctctctctctctctctctctctctctctctcc 1127
Qy 862 ccttataatatacattaggaacaagaggttaaaaggaagctttaaaaggttggtgcaag 921
Db 1128 ttcatctacaccttgaggaataagagcgtgaagagctctccgaagactcctgcaag 1187

RESULT 14

US-09-546-986A-5
; Sequence 5, Application US/09546986A
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Novel G-Protein Coupled Receptors
; FILE REFERENCE: 018781-004720US
; CURRENT APPLICATION NUMBER: US/09/546,986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 1351
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (86)..(1108)
; OTHER INFORMATION: human breast cancer amplified G-protein coupled
; OTHER INFORMATION: receptor 3 (BCA-GPCR-3)
US-09-546-986A-5

Query Match 33.9%; Score 319.6; DB 5; Length 1351;
Best Local Similarity 59.8%; Pred. No. 9e-80;
Matches 535; Conservative 0; Mismatches 359; Indels 0; Gaps 0;

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RESULT 15

US-09-981-566A-27
; Sequence 27, Application US/09981566A
; GENERAL INFORMATION:
; APPLICANT: Kekuda et al.
; TITLE OF INVENTION: Novel GPCR-like Proteins and Nucleic Acids Encoding
; FILE REFERENCE: 21402-163
; CURRENT APPLICATION NUMBER: US/09/981,566A
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 60/240,704
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/262,159
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/263,340
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/264,118
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/308,203
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/243,497
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/244,542
; PRIOR FILING DATE: 2000-10-31
; PRIOR APPLICATION NUMBER: 60/269,031
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: 60/245,484
; PRIOR FILING DATE: 2000-11-03
; PRIOR APPLICATION NUMBER: 60/255,017
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 60/263,216
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/268,225
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 209
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 971
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-981-566A-27

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QY	62 ccttgctggagtttccacctctgtgtctcttgaatttcttaacctgtacacctt 121				
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DB	186 ttcttctctgcacacctctctctctcttgacatgagcttcacacagacatgttccacag 245				
QY	242 atgctaagtaattatgacagatcagcaagtaacagttatctgtgctgtgtagccag 301				
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QY	302 ctttcatattctggccttgggggtactgaatatcttctctgcgcgtcatgtcctt 361				
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DB	366 gaccgctacgctgcacatcgagccactccattacactgtcatatgcatcaccagctt 425				
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QY	482 accctgactctcagctgcaactctgtgaccccatgtgatagatcacttctctgtgaa 541				
DB	486 acgctcaccaatgctcctacacgctgtgtgggaacaattgcatcgacacactcttgcgag 545				
QY	542 gtccctgacagctgcaagttatctgtgtgtgagacacagcaaatgaggtgaactatc 601				
DB	546 atgcccctcaatgacactgtgctgtgtgataccagcctcaatgagatgagatgtac 605				
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Search completed: August 25, 2002, 19:09:40
Job time: 4483 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 25, 2002, 19:09:47 ; Search time 217.52 Seconds

(without alignments)
506,482 Million cell updates/sec

Title: US-09-800-321A-4

Perfect score: 1607
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Sequence: BLOSUM62
Gapop 10.0 , Gapext 0.5

Scoring table: 3502263 segs, 351980561 residues

Searched: Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1593	99.1	313	21	US-09-755-017-2
3	1593	99.1	313	21	US-09-795-271-74
4	1593	99.1	313	22	US-09-800-321A-74
5	1593	99.1	313	22	US-09-800-321A-34
6	1593	99.1	313	22	US-09-809-476-74
7	1593	99.1	313	23	US-09-924-359-232

8	1586	98.7	313	22	US-09-800-321A-6	Sequence 6, Appl1
9	1299	80.8	357	21	US-09-795-271-75	Sequence 75, Appl1
10	1299	80.8	357	22	US-09-800-321A-35	Sequence 35, Appl1
11	1299	80.8	357	22	US-09-809-476-75	Sequence 75, Appl1
12	1299	80.8	357	23	US-09-912-976-57	Sequence 57, Appl1
13	1299	80.8	357	23	US-09-912-976-63	Sequence 63, Appl1
14	1295	80.6	310	21	US-09-795-271-77	Sequence 77, Appl1
15	1295	80.6	310	22	US-09-800-321A-36	Sequence 36, Appl1
16	1295	80.6	310	22	US-09-809-476-77	Sequence 77, Appl1
17	1295	80.6	357	21	US-09-795-271-76	Sequence 76, Appl1
18	1295	80.6	357	22	US-09-800-321A-37	Sequence 37, Appl1
19	1295	80.6	357	22	US-09-809-476-76	Sequence 76, Appl1
20	1295	80.6	357	23	US-09-912-976-58	Sequence 58, Appl1
21	1295	80.6	357	23	US-09-912-976-65	Sequence 65, Appl1
22	1295	80.6	357	23	US-09-924-359-142	Sequence 142, Appl1
23	1259	78.3	313	21	US-09-779-679-62	Sequence 62, Appl1
24	1259	78.3	313	21	US-09-795-271-73	Sequence 73, Appl1
25	1259	78.3	313	22	US-09-809-476-73	Sequence 73, Appl1
26	1259	78.3	313	22	US-09-912-976-62	Sequence 62, Appl1
27	1259	78.3	313	23	US-09-924-359-143	Sequence 143, Appl1
28	1247	77.6	313	21	US-09-779-679-55	Sequence 55, Appl1
29	1139	70.9	280	22	US-09-800-321A-38	Sequence 38, Appl1
30	1123	69.9	504	26	US-60-248-505-940	Sequence 940, Appl
31	1034	64.3	203	22	US-09-800-321A-41	Sequence 41, Appl1
32	1003	62.4	199	26	US-60-178-308-2276	Sequence 2276, Ap
33	953	59.3	692	26	US-60-258-250-110	Sequence 110, App
34	948	59.0	440	26	US-60-245-225-321	Sequence 321, App
35	948	59.0	440	26	US-60-258-250-97	Sequence 97, Appl
36	944.5	58.8	327	21	US-09-795-271-29	Sequence 29, Appl
37	944.5	58.8	327	22	US-09-809-476-29	Sequence 29, Appl
38	939	58.4	310	19	US-09-524-730-2	Sequence 2, Appl1
39	939	58.4	310	24	US-10-028-512-2	Sequence 2, Appl1
40	937	58.3	312	23	US-09-924-359-2	Sequence 2, Appl1
41	937	58.3	312	23	US-09-924-359-4	Sequence 4, Appl1
42	936	58.2	309	23	US-09-912-976-16	Sequence 16, Appl
43	936	58.2	309	24	US-10-034-842-7	Sequence 7, Appl1
44	936	58.2	309	26	US-60-207-360-335	Sequence 335, App
45	936	58.2	309	26	US-60-301-751-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-800-321A-4
: Sequence 4, Application US/09800321A
: GENERAL INFORMATION:
: APPLICANT: Padigaru, Muralihara
: APPLICANT: Burgess, Catherine E
: APPLICANT: Mishra, Vishnu
: APPLICANT: Li, Li
: APPLICANT: Baumgartner, Jason C
: APPLICANT: Majumder, Kundu
: APPLICANT: Szytek, Kimberly A
: APPLICANT: Tcherenev, Vellizar T
: TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 15966-703 US
: CURRENT APPLICATION NUMBER: US/09/800,321A
: CURRENT FILING DATE: 2001-03-05
: PRIOR APPLICATION NUMBER: 60/186,606
: PRIOR FILING DATE: 2000-03-03
: PRIOR APPLICATION NUMBER: 60/221,942
: PRIOR FILING DATE: 2000-07-31
: PRIOR APPLICATION NUMBER: 60/260,285
: PRIOR FILING DATE: 2001-01-08
: PRIOR APPLICATION NUMBER: 60/220,263
: PRIOR FILING DATE: 2000-07-24
: PRIOR APPLICATION NUMBER: 60/257,600
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/187,295
: PRIOR FILING DATE: 2000-03-06
: PRIOR APPLICATION NUMBER: 60/219,854
: PRIOR FILING DATE: 2000-07-21

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;; PRIOR APPLICATION NUMBER: 60/187,249
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: 60/187,247
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: 60/187,250
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: 60/187,253
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: 60/187,248
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: 60/187,296
;; PRIOR FILING DATE: 2000-03-06
;; PRIOR APPLICATION NUMBER: 60/187,563
;; PRIOR FILING DATE: 2000-03-07
;; NUMBER OF SEQ ID NOS: 78
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 313
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-800-321a-4
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Best Local Similarity 100.0%; Pred. No. 5.1e-145;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-755-017-2
;; Sequence 2, Application US/09755017
;; GENERAL INFORMATION:
;; APPLICANT: Walke, D. Wade
;; APPLICANT: Wilganowski, Nathaniel
;; APPLICANT: Turner, C. Alexander Jr.
;; APPLICANT: Friedrich, Glenn
;; APPLICANT: Abulu, Alejandro
;; APPLICANT: Zambrowicz, Brian
;; APPLICANT: Sands, Arthur T.
;; TITLE OF INVENTION: Novel Human Membrane Proteins and
;; FILE REFERENCE: LEX-0115-USA
;; CURRENT APPLICATION NUMBER: US/09/755,017
;; PRIOR FILING DATE: 2001-01-05
;; PRIOR APPLICATION NUMBER: US 60/175,764
;; PRIOR FILING DATE: 2000-01-12
;; NUMBER OF SEQ ID NOS: 3
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2
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;; LENGTH: 313
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-755-017-2
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Query Match          99.1%; Score 1593; DB 21; Length 313;
Best Local Similarity 99.7%; Pred. No. 1.1e-143;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 3
US-09-795-271-74
;; Sequence 74, Application US/09795271
;; GENERAL INFORMATION:
;; APPLICANT: Padigaru, Muralidhara
;; APPLICANT: Majumder, Kumud
;; APPLICANT: Burgess, Catherine E
;; APPLICANT: Vernet, Corine A.M
;; APPLICANT: Fernandes, Elma
;; APPLICANT: Shmukets, Richard A
;; APPLICANT: Tcherenev, Velizar T
;; APPLICANT: Mishra, Vishnu
;; APPLICANT: Casman, Stacie
;; APPLICANT: Szytek, Kimberly A
;; APPLICANT: Zernhusen, Bryan
;; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
;; FILE REFERENCE: 15966-694
;; CURRENT APPLICATION NUMBER: US/09/795,271
;; PRIOR FILING DATE: 2001-02-27
;; PRIOR APPLICATION NUMBER: 60/185,674
;; PRIOR FILING DATE: 2000-02-28
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; PRIOR APPLICATION NUMBER: 60/260,020
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/264,849
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/186,715
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 74
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-271-74
```

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Query Match          99.1%; Score 1593; DB 21; Length 313;
Best Local Similarity 99.7%; Pred. No. 1,1e-143;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MNVNDSTIOEFLILGSDRPMLEFPLLVFLISYTVTFICNLTIIIVSRIDTKLHTPMY 60
   1 MNVNDSTIOEFLILGSDRPMLEFPLLVFLISYTVTFICNLTIIIVSRIDTKLHTPMY 60
Db 1 MNVNDSTIOEFLILGSDRPMLEFPLLVFLISYTVTFICNLTIIIVSRIDTKLHTPMY 60
QY 61 FFELNLSLIDLCYTCCTVPMQVNLCSIRKVISYRGCAQLFIFLAGATEYLLAVMSF 120
   61 FFELNLSLIDLCYTCCTVPMQVNLCSIRKVISYRGCAQLFIFLAGATEYLLAVMSF 120
Db 61 FFELNLSLIDLCYTCCTVPMQVNLCSIRKVISYRGCAQLFIFLAGATEYLLAVMSF 120
QY 121 DWEFAICRPLHYSYMQRICLQLAASWYGFNSWMLSTLTQLDPLCDPYVIDHFLCE 180
   121 DWEFAICRPLHYSYMQRICLQLAASWYGFNSWMLSTLTQLDPLCDPYVIDHFLCE 180
Db 121 DWEFAICRPLHYSYMQRICLQLAASWYGFNSWMLSTLTQLDPLCDPYVIDHFLCE 180
QY 181 VPALKISCVEETANEAEFLVSELFHLIPLTLLISYAFIVRAVLRIOSEGRQKAFGT 240
   181 VPALKISCVEETANEAEFLVSELFHLIPLTLLISYAFIVRAVLRIOSEGRQKAFGT 240
Db 181 VPALKISCVEETANEAEFLVSELFHLIPLTLLISYAFIVRAVLRIOSEGRQKAFGT 240
QY 241 CGSHLIYVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPITYTLRNKKEVKEG 300
   241 CGSHLIYVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPITYTLRNKKEVKEG 300
Db 241 CGSHLIYVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPITYTLRNKKEVKEG 300
QY 301 FKRLVARVFLIKK 313
   301 FKRLVARVFLIKK 313
Db 301 FKRLVARVFLIKK 313
```

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RESULT 4
US-09-800-321A-2
; Sequence 2, Application US/09800321A
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Burgess, Catherine E
; APPLICANT: Mishra, Vishnu
; APPLICANT: Li, Li
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Majumder, Kumud
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Tcherenev, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-703 US
; CURRENT APPLICATION NUMBER: US/09/800,321A
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,606
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/221,942
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/260,285
; PRIOR FILING DATE: 2001-01-08
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; PRIOR APPLICATION NUMBER: 60/220,263
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/257,600
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/187,295
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/219,854
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/187,249
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,247
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,250
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,253
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,248
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,296
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,563
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 2
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-321A-2
```

```
Query Match          99.1%; Score 1593; DB 22; Length 313;
Best Local Similarity 99.7%; Pred. No. 1,1e-143;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MNVNDSTIOEFLILGSDRPMLEFPLLVFLISYTVTFICNLTIIIVSRIDTKLHTPMY 60
   1 MNVNDSTIOEFLILGSDRPMLEFPLLVFLISYTVTFICNLTIIIVSRIDTKLHTPMY 60
Db 1 MNVNDSTIOEFLILGSDRPMLEFPLLVFLISYTVTFICNLTIIIVSRIDTKLHTPMY 60
QY 61 FFELNLSLIDLCYTCCTVPMQVNLCSIRKVISYRGCAQLFIFLAGATEYLLAVMSF 120
   61 FFELNLSLIDLCYTCCTVPMQVNLCSIRKVISYRGCAQLFIFLAGATEYLLAVMSF 120
Db 61 FFELNLSLIDLCYTCCTVPMQVNLCSIRKVISYRGCAQLFIFLAGATEYLLAVMSF 120
QY 121 DWEFAICRPLHYSYMQRICLQLAASWYGFNSWMLSTLTQLDPLCDPYVIDHFLCE 180
   121 DWEFAICRPLHYSYMQRICLQLAASWYGFNSWMLSTLTQLDPLCDPYVIDHFLCE 180
Db 121 DWEFAICRPLHYSYMQRICLQLAASWYGFNSWMLSTLTQLDPLCDPYVIDHFLCE 180
QY 181 VPALKISCVEETANEAEFLVSELFHLIPLTLLISYAFIVRAVLRIOSEGRQKAFGT 240
   181 VPALKISCVEETANEAEFLVSELFHLIPLTLLISYAFIVRAVLRIOSEGRQKAFGT 240
Db 181 VPALKISCVEETANEAEFLVSELFHLIPLTLLISYAFIVRAVLRIOSEGRQKAFGT 240
QY 241 CGSHLIYVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPITYTLRNKKEVKEG 300
   241 CGSHLIYVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPITYTLRNKKEVKEG 300
Db 241 CGSHLIYVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPITYTLRNKKEVKEG 300
QY 301 FKRLVARVFLIKK 313
   301 FKRLVARVFLIKK 313
Db 301 FKRLVARVFLIKK 313
```

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RESULT 5
US-09-800-321A-34
; Sequence 34, Application US/09800321A
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Burgess, Catherine E
; APPLICANT: Mishra, Vishnu
; APPLICANT: Li, Li
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Majumder, Kumud
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Tcherenev, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
```

```
FILE REFERENCE: 15966-703 US
CURRENT APPLICATION NUMBER: US/09/800,321A
CURRENT FILING DATE: 2001-03-05
PRIOR APPLICATION NUMBER: 60/186,606
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/221,942
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 60/260,285
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/220,263
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/257,600
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/187,295
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/219,854
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 60/187,249
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/187,247
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/187,250
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/187,253
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/187,248
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/187,296
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: 60/187,563
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 34
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-321a-34

Query Match          99.1%; Score 1593; DB 22; Length 313;
Best Local Similarity 99.7%; Pred. No. 1,1e-143;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNWVNDIIIOEFILGFSDRPMLFPLLVFLISYTVTIFGNLTIIIVSRDTRKLTHTPMY 60
DB 1 MNWVNDIIIOEFILGFSDRPMLFPLLVFLISYTVTIFGNLTIIIVSRDTRKLTHTPMY 60
QY 61 FELTNLSLDDCYTTCVPMQMLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
DB 61 FELTNLSLDDCYTTCVPMQMLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
QY 121 DMFVAICRPLHYIVIMHORCLQOLAASWYTGFSNSYWLSTFLQPLCDPYVIDHFLCE 180
DB 121 DMFVAICRPLHYIVIMHORCLQOLAASWYTGFSNSYWLSTFLQPLCDPYVIDHFLCE 180
QY 121 DMFVAICRPLHYIVIMHORCLQOLAASWYTGFSNSYWLSTFLQPLCDPYVIDHFLCE 180
DB 121 DMFVAICRPLHYIVIMHORCLQOLAASWYTGFSNSYWLSTFLQPLCDPYVIDHFLCE 180
QY 181 VPALKLSCVETTANEAELFVSELPHILPILITLISYAFIVRAVLRIQSAEGRQAKFGT 240
DB 181 VPALKLSCVETTANEAELFVSELPHILPILITLISYAFIVRAVLRIQSAEGRQAKFGT 240
QY 241 CGSHLIIVSVLFYSTAVSVYIQPPSPSSKDGKMSLFGYGIAPMLNPLIYTLRKKEVKEG 300
DB 241 CGSHLIIVSVLFYSTAVSVYIQPPSPSSKDGKMSLFGYGIAPMLNPLIYTLRKKEVKEG 300
QY 301 FKRLVAVRFLIKK 313
DB 301 FKRLVAVRFLIKK 313

RESULT 6
US-09-800-476-74
; Sequence 74, Application us/09809476
; GENERAL INFORMATION:
```

```
APPLICANT: Padigaru, Muralidhara
APPLICANT: Majumder, Kumud
APPLICANT: Burgess, Catherine E
APPLICANT: Vernet, Corine A.M
APPLICANT: Fernandes, Elma
APPLICANT: Shinkets, Richard A
APPLICANT: Tchernev, Velizar T
APPLICANT: Mishra, Vishnu
APPLICANT: Casman, Stacie
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 15966-694CIP
CURRENT APPLICATION NUMBER: US/09/809,476
CURRENT FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: 60/185,674
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/185,535
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: 60/186,585
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/186,604
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/186,584
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/186,717
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/186,716
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/186,719
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/186,827
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 60/218,323
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/218,435
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/220,517
PRIOR FILING DATE: 2000-07-24
PRIOR APPLICATION NUMBER: 60/223,897
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 60/260,020
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/264,849
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: 60/186,715
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: 09/795,271
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 60/259,031
PRIOR FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 74
LENGTH: 313
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-476-74

Query Match          99.1%; Score 1593; DB 22; Length 313;
Best Local Similarity 99.7%; Pred. No. 1,1e-143;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNWVNDIIIOEFILGFSDRPMLFPLLVFLISYTVTIFGNLTIIIVSRDTRKLTHTPMY 60
DB 1 MNWVNDIIIOEFILGFSDRPMLFPLLVFLISYTVTIFGNLTIIIVSRDTRKLTHTPMY 60
QY 61 FELTNLSLDDCYTTCVPMQMLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
DB 61 FELTNLSLDDCYTTCVPMQMLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
QY 121 DMFVAICRPLHYIVIMHORCLQOLAASWYTGFSNSYWLSTFLQPLCDPYVIDHFLCE 180
DB 121 DMFVAICRPLHYIVIMHORCLQOLAASWYTGFSNSYWLSTFLQPLCDPYVIDHFLCE 180
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Db 121 DRFVALICRPLHYSYIMQRIQLQAAASWYGFNSWVSTLTLLQPLCDPYVIDHFLCE 180
QY 181 VPALLKISCVEETANAEELFVSELFHLIPLTLLISYAFIVRAVRIQSAEGROKAFGT 240
Db 181 VPALLKISCVEETANAEELFVSELFHLIPLTLLISYAFIVRAVRIQSAEGROKAFGT 240
QY 241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKKEVKEG 300
Db 241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKKEVKEG 300
QY 301 FKRLVARVFLIKK 313
Db 301 FKRLVARVFLIKK 313

```

```

RESULT 7
US-09-924-359-232
; Sequence 232, Application US/09924359
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Baumgartner, Jason
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Verneil, Corine
; APPLICANT: Ballinger, Robert A
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Burgess, Catherine E
; APPLICANT: Mezes, Peter S
; APPLICANT: Grosse, William M
; APPLICANT: Alsobrook II, John P
; APPLICANT: Gorman, Linda
; APPLICANT: LaRoche, William J
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Colman, Steven D
; APPLICANT: Szekeres Jr, Edward S
; FILE REFERENCE: 21402-078
; TITLE OF INVENTION: Novel Proteins And Nucleic Acids Encoding Same
; CURRENT APPLICATION NUMBER: US/09/924,359
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/223,472
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/223,138
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/224,613
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/224,815
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/260,003
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,072
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,283
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/260,450
; PRIOR FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/261,156
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: 60/263,338
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/263,434
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/265,704
; PRIOR FILING DATE: 2001-02-01
; PRIOR APPLICATION NUMBER: 60/269,964
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: 60/274,873
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/276,406
; PRIOR FILING DATE: 2001-03-15

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; PRIOR APPLICATION NUMBER: 60/287,916
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 427
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 232
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-924-359-232

```

```

Query Match          99.1%; Score 1593; DB 23; Length 313;
Best Local Similarity 99.7%; Pred. No. 1,1e-143;
Matches 312; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 MNWVNDSTIOEFILGSDRPMLEFLLVFLISYTYTIFGNLTIIIVSRIDYKHPMY 60
Db 1 MNWVNDSTIOEFILGSDRPMLEFLLVFLISYTYTIFGNLTIIIVSRIDYKHPMY 60
QY 61 FFLTNLSLDLCYTTCTVPQMLVNLCSIRKVISYRGCAQLFPLALGATEYLLAVMSF 120
Db 61 FFLTNLSLDLCYTTCTVPQMLVNLCSIRKVISYRGCAQLFPLALGATEYLLAVMSF 120
QY 121 DWFVALICRPLHYSYIMQRIQLQAAASWYGFNSWVSTLTLLQPLCDPYVIDHFLCE 180
Db 121 DWFVALICRPLHYSYIMQRIQLQAAASWYGFNSWVSTLTLLQPLCDPYVIDHFLCE 180
QY 181 VPALLKISCVEETANAEELFVSELFHLIPLTLLISYAFIVRAVRIQSAEGROKAFGT 240
Db 181 VPALLKISCVEETANAEELFVSELFHLIPLTLLISYAFIVRAVRIQSAEGROKAFGT 240
QY 241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKKEVKEG 300
Db 241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKKEVKEG 300
QY 301 FKRLVARVFLIKK 313
Db 301 FKRLVARVFLIKK 313

```

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RESULT 8
US-09-800-321A-6
; Sequence 6, Application US/09800321A
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Burgess, Catherine E
; APPLICANT: Mishra, Vishnu
; APPLICANT: Li, Li
; APPLICANT: Baumgartner, Jason C
; APPLICANT: Majumder, Kumud
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-703 US
; CURRENT APPLICATION NUMBER: US/09/800,321A
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,606
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/221,942
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 60/260,285
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/220,263
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/257,600
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/187,295
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/219,854
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 60/187,249
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,247

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; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,250
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,253
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,248
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,296
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: 60/187,563
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-321a-6
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```
Query Match          98.7%; Score 1586; DB 22; Length 313;
Best Local Similarity 99.0%; Pred. No. 5,2e-143;
Matches 310; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 1 MNNVNDIIIOFFILGSDRPMLEFPLLVFLISYTVTIGNTLIIIVSRDLTKLHPTMY 60
D 1 MNNVNDIIIOFFILGSDRPMLEFPLLVFLISYTVTIGNTLIIIVSRDLTKLHPTMY 60
QY 61 FFLTNLSLDDCYTTCVPPQMLVNLCSIRKVISYRGCAQLFTFLALGATEYLLAVMSF 120
D 61 FFLTNLSLDDCYTTCVPPQMLVNLCSIRKVISYRGCAQLFTFLALGATEYLLAVMSF 120
QY 121 DMFVAICRPLHYSHIMQRCLQLAAASWVTGFSNSVWLSLTQLPLCDPYVIDHFLCE 180
D 121 DMFVAICRPLHYSHIMQRCLQLAAASWVTGFSNSVWLSLTQLPLCDPYVIDHFLCE 180
QY 181 VPALKIKSCVETTANAEELFVSEFLHILPILITLIIISYATFVRAVLRIQSAEGRKAFT 240
D 181 VPALKIKSCVETTANAEELFVSEFLHILPILITLIIISYATFVRAVLRIQSAEGRKAFT 240
QY 241 CGSHLIVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVEKG 300
D 241 CGSHLIVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVEKG 300
QY 301 FKRLVAVFLIKK 313
D 301 FKRLVAVFLIKK 313

RESULT 9
US-09-795-271-75
; Sequence 75, Application US/09795271
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Padigaru, Kumud
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkets, Richard A
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Mishra, Vishnu
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly A
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-694
; CURRENT APPLICATION NUMBER: US/09/795,271
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 60/185,674
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,535
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,585
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; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/186,604
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/186,584
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/186,717
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/186,716
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/186,719
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/186,827
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/218,323
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/218,435
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/220,517
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: 60/223,897
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: 60/260,020
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/264,849
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: 60/186,715
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-271-75
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```
Query Match          80.8%; Score 1299; DB 21; Length 357;
Best Local Similarity 81.6%; Pred. No. 1,8e-115;
Matches 253; Conservative 24; Mismatches 33; Indels 0; Gaps 0;
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QY 1 MNNVNDIIIOFFILGSDRPMLEFPLLVFLISYTVTIGNTLIIIVSRDLTKLHPTMY 60
D 1 MNNVNDIIIOFFILGSDRPMLEFPLLVFLISYTVTIGNTLIIIVSRDLTKLHPTMY 60
QY 61 FFLTNLSLDDCYTTCVPPQMLVNLCSIRKVISYRGCAQLFTFLALGATEYLLAVMSF 120
D 61 FFLTNLSLDDCYTTCVPPQMLVNLCSIRKVISYRGCAQLFTFLALGATEYLLAVMSF 120
QY 121 DMFVAICRPLHYSHIMQRCLQLAAASWVTGFSNSVWLSLTQLPLCDPYVIDHFLCE 180
D 121 DMFVAICRPLHYSHIMQRCLQLAAASWVTGFSNSVWLSLTQLPLCDPYVIDHFLCE 180
QY 181 VPALKIKSCVETTANAEELFVSEFLHILPILITLIIISYATFVRAVLRIQSAEGRKAFT 240
D 181 VPALKIKSCVETTANAEELFVSEFLHILPILITLIIISYATFVRAVLRIQSAEGRKAFT 240
QY 241 CGSHLIVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVEKG 300
D 241 CGSHLIVSLFYSTAVSVYIQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVEKG 300
QY 301 FKRLVAVFL 310
D 301 FKRLVAVFL 310

RESULT 10
US-09-800-321a-35
; Sequence 35, Application US/09800321A
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Padigaru, Burgess, Catherine E
; APPLICANT: Mishra, Vishnu
; APPLICANT: Li, Li
```



```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-795-271-77

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1 Sequence 36 Application US/059800321A
2 GENERAL INFORMATION:
3 APPLICANT: Padigaru, Muralidhara
4 APPLICANT: Burgess, Catherine E
5 APPLICANT: Mishra, Vishnu
6 APPLICANT: Li, Li
7 APPLICANT: Baumgartner, Jason C
8 APPLICANT: Majumder, Kunud
9 APPLICANT: Spytek, Kimberly A
10 APPLICANT: Tchiernev, Velizar T
11 TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
12 FILE REFERENCE: 15966-703 US
13 CURRENT APPLICATION NUMBER: US/09/800,321A
14 CURRENT FILING DATE: 2001-03-05
15 PRIOR APPLICATION NUMBER: 60/186,606
16 PRIOR FILING DATE: 2000-03-03
17 PRIOR APPLICATION NUMBER: 60/221,942
18 PRIOR FILING DATE: 2000-07-31
19 PRIOR APPLICATION NUMBER: 60/260,285
20 PRIOR FILING DATE: 2001-01-08
21 PRIOR APPLICATION NUMBER: 60/220,263
22 PRIOR FILING DATE: 2000-07-24
23 PRIOR APPLICATION NUMBER: 60/257,600
24 PRIOR FILING DATE: 2000-12-21
25 PRIOR APPLICATION NUMBER: 60/187,295
26 PRIOR FILING DATE: 2000-03-06
27 PRIOR APPLICATION NUMBER: 60/219,854
28 PRIOR FILING DATE: 2000-07-21
29 PRIOR APPLICATION NUMBER: 60/187,249
30 PRIOR FILING DATE: 2000-03-06
31 PRIOR APPLICATION NUMBER: 60/187,247
32 PRIOR FILING DATE: 2000-03-06
33 PRIOR APPLICATION NUMBER: 60/187,250
34 PRIOR FILING DATE: 2000-03-06
35 PRIOR APPLICATION NUMBER: 60/187,253
36 PRIOR FILING DATE: 2000-03-06
37 PRIOR APPLICATION NUMBER: 60/187,248
38 PRIOR FILING DATE: 2000-03-06
39 PRIOR APPLICATION NUMBER: 60/187,296
40 PRIOR FILING DATE: 2000-03-06
41 PRIOR APPLICATION NUMBER: 60/187,563
42 PRIOR FILING DATE: 2000-03-07

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; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-321A-36

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Query Match      80.6% Score 1295; DB 22: Length 310;
Best Local Similarity 81.3% Pred No. 3.8e-115;
Matches 252; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

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QY 1 MMWVNDSTIQEFLILGFSDRPMLLEPPLAVFLISYVTITFGNLTITLVSRLDTKLTTPMY 60
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
DB 1 MMWVNSVPOEFILLVFSQPMLEIPPEVFMFLFSYILITFGNLTITLVSRLDTKLTTPMY 60
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
QY 61 FFLTNLSLDLCYTTCTVQMLVNLCSIRKVISYRCVQAQLFIFLALGATEYILLAVMSF 120
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
DB 61 FFLSNLSLDLCYTTSTVPQMLVNLCSIRKVISYRCVQAQLFIFLALGATEYILLAVMSF 120
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
QY 121 DMFVAICRPLHYSVIMHQRICQLAAASWVTGFSNSVLTSLTLOLPICDPYVIDHFICE 180
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
DB 121 DMFVAICRPLHYSVIMHQRICQLAAASWVTGFSNSVLTSLTLOLPICDPYVIDHFICE 180
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
QY 181 VPALLKLSCEVTANEAEELFLVSEFLPLPLILISYAFIVRAVLRISAEGRQKAFGT 240
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
DB 181 VPALLKLSCEVTANEAEELFLVSEFLPLPLILISYAFIVRAVLRISAEGRQKAFGT 240
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
QY 241 CGSHLIVSLFYSTANVSVLQPPSPSSKDGKWSLFGIITAPMLNPLIYTLRNKEVKEG 300
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
DB 241 CGSHLIVSLFYSTANVSVLQPPSPSSKDGKWSLFGIITAPMLNPLIYTLRNKEVKEG 300
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
QY 301 FKRIVARVFL 310
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||
DB 301 FKRIVAKSL 310
   ||||| : ||||| ||| : ||| : ||||| ||||| : |||||

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Search completed: August 25, 2002, 20:12:51
Job time: 3784 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 25, 2002, 20:07:17 ; Search time 133.9 Seconds

(without alignments)
558,742 Million cell updates/sec

Title: US-09-800-321A-4

Perfect score: 1607
Sequence: 1 MMWVDSIIQEFILGFSDR.....NKEVGEGRKLVARVFLIK 313Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 73335 segs, 239027266 residues

Total number of hits satisfying chosen parameters: 733335

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:*

- 1: /cgn2_6/ptodata/2/paa/PCT_US06_NEW_COMB.pep:*
- 2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB	ID	Description
1	1299	80.8	357	5	US-09-965-422-50	Sequence 50, Appl
2	1299	80.8	357	5	US-09-907-218-46	Sequence 46, Appl
3	1295	80.6	310	5	US-09-907-218-49	Sequence 49, Appl
4	1295	80.6	357	5	US-09-965-422-52	Sequence 52, Appl
5	1295	80.6	357	5	US-09-907-218-48	Sequence 48, Appl
6	1295	80.6	357	5	US-10-032-189-112	Sequence 112, Appl
7	1259	78.3	313	5	US-09-965-422-44	Sequence 44, Appl
8	1259	78.3	313	5	US-09-907-218-45	Sequence 45, Appl
9	1259	78.3	313	5	US-09-907-218-79	Sequence 79, Appl
10	1130	70.3	313	5	US-09-981-566A-70	Sequence 70, Appl
11	947	58.9	318	1	PCT-US02-03635-48	Sequence 48, Appl
12	939	58.4	310	5	US-09-546-986A-2	Sequence 2, Appl
13	936	58.2	309	1	PCT-US02-03635-32	Sequence 32, Appl
14	936	58.2	309	5	US-09-965-422-12	Sequence 12, Appl
15	935	58.2	309	6	US-10-032-189-111	Sequence 11, Appl
16	935	58.2	312	6	US-10-032-189-34	Sequence 34, Appl
17	933	58.1	311	5	US-09-981-566A-32	Sequence 32, Appl
18	933	57.9	312	6	US-10-032-106-7	Sequence 7, Appl
19	931	57.9	312	6	US-10-032-189-109	Sequence 109, Appl
20	917	57.1	312	5	US-09-981-566A-30	Sequence 30, Appl
21	915	56.9	312	5	US-09-981-566A-31	Sequence 31, Appl
22	908	56.5	310	5	US-09-965-422-47	Sequence 47, Appl
23	902	56.1	312	5	US-09-965-422-49	Sequence 49, Appl
24	902	56.1	312	5	US-09-907-218-47	Sequence 47, Appl
25	902	56.1	312	5	US-09-907-218-78	Sequence 78, Appl
26	902	56.1	312	5	US-09-981-566A-29	Sequence 29, Appl

27	891	55.4	334	5	US-09-965-422-10	Sequence 10, Appl
28	889	55.3	312	5	US-09-965-422-46	Sequence 46, Appl
29	886	55.1	317	1	PCT-US02-03635-11	Sequence 11, Appl
30	885	55.1	316	5	US-09-965-422-45	Sequence 45, Appl
31	884	55.0	334	5	US-09-965-422-4	Sequence 4, Appl
32	883	54.9	312	6	US-10-002-945-98	Sequence 98, Appl
33	883	54.9	334	5	US-09-965-422-6	Sequence 6, Appl
34	883	54.9	334	5	US-09-965-422-8	Sequence 8, Appl
35	883	54.9	334	5	US-09-546-986A-8	Sequence 8, Appl
36	879	54.7	320	5	US-09-546-986A-6	Sequence 6, Appl
37	876	54.5	320	5	US-09-981-566A-28	Sequence 28, Appl
38	875	54.4	319	1	PCT-US02-09923-39	Sequence 39, Appl
39	871	54.2	320	5	US-09-981-566A-33	Sequence 33, Appl
40	871	54.2	320	6	US-10-032-189-113	Sequence 113, Appl
41	867	54.0	317	5	US-09-965-422-51	Sequence 51, Appl
42	865	53.8	312	5	US-09-965-422-48	Sequence 48, Appl
43	855.5	53.2	311	1	PCT-US02-09923-33	Sequence 33, Appl
44	855.5	53.2	311	5	US-09-907-218-10	Sequence 10, Appl
45	825.5	51.4	311	6	US-10-023-601-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
US-09-965-422-50
Sequence 50, Application US/09965422
GENERAL INFORMATION:
APPLICANT: Spytek, Kimberly A
APPLICANT: Casman, Stacie
APPLICANT: Padigaru, Muralidhara
APPLICANT: Dickson, Kevin
APPLICANT: Vernet, Corline
APPLICANT: Spaderna, Steven K
APPLICANT: Shenoy, Suresh G
APPLICANT: Gerlach, Valerie
APPLICANT: Ellerman, Karen
APPLICANT: Edinger, Shlomit
APPLICANT: MacDougall, John R
APPLICANT: Smithson, Glenda
APPLICANT: Li, Li
APPLICANT: Malyankar, Urtil M
APPLICANT: Taylor, Sarah
APPLICANT: Gunther, Erik
APPLICANT: Tchiernev, Velizar T
TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21401-132
CURRENT APPLICATION NUMBER: US/09/965,422
PRIOR FILING DATE: 2001-09-27, 286
PRIOR APPLICATION NUMBER: 60/236, 284
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: 60/237, 581
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/238, 735
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/240, 736
PRIOR FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: 60/260, 019
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: 60/260, 338
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/262, 156
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/262, 498
PRIOR FILING DATE: 2001-01-18
PRIOR APPLICATION NUMBER: 60/263, 133
PRIOR FILING DATE: 2001-01-19
PRIOR APPLICATION NUMBER: 60/263, 691
PRIOR FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: 60/266, 109
PRIOR FILING DATE: 2001-02-02

;; PRIOR APPLICATION NUMBER: 60/271,634
;; PRIOR FILING DATE: 2001-02-26
;; NUMBER OF SEQ ID NOS: 127
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 50
;; LENGTH: 357
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-965-422-50

Query Match 80.8%; Score 1299; DB 5; Length 357;
Best Local Similarity 81.6%; Pred. No. 6.1e-96;
Matches 253; Conservative 24; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNWVNDSTIOEIIIGFSDRPWLEFPPLVVLISYTVTFGNLTIIIVSRDLTKLHPMY 60
DB 1 MNWVNSVQGEFILLVFSDDQWLEIPFVWMLFYSYILTFGNLTIIIVSHVDFKLHPMY 60
QY 61 FFLNLSLDDCTTCTTCYVPMVLNLCSTIRKVISYGCVAQOLFIFLALGATEYLLAVWSF 120
DB 61 FFLNLSLDDCTTCTTCYVPMVLNLCSTIRKVISYGCVAQOLFIFLALGATEYLLAVWSF 120
QY 121 DMFAICRPLHYSTMORLCLOLAASWVGFNSVWLSITLITOLPLCDYVIDHFCE 180
DB 121 DMFAICRPLHYSTMORLCLOLAASWVGFNSVWLSITLITOLPLCDYVIDHFCE 180
QY 181 VPALLKSCVETANEAELEFVSELFLIPLTLILISYAFIVRAVLRIOSEGRKAFGT 240
DB 181 VPALLKSCVETANEAELEFVSELFLIPLTLILISYAFIVRAVLRIOSEGRKAFGT 240
QY 241 CGSHLIYVSLEYFAYISWYLOPPSPSSKDGKMSLFYGIAPMLNPLIYLRNKEVEG 300
DB 241 CGSHLIYVSLEYFAYISWYLOPPSPSSKDGKMSLFYGIAPMLNPLIYLRNKEVEG 300
QY 301 FKRLVAVFL 310
DB 301 FKRLVAVFL 310

RESULT 2
; Sequence 46, Application US/09907218
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patnrajan, Meera
; APPLICANT: Tallon, Bruce
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam Ryan
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly Ann
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-061
; CURRENT APPLICATION NUMBER: US/09/907, 218
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/218,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/260,977
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/263,801
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/268,226
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/271,622
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-907-218-46

Query Match 80.8%; Score 1299; DB 5; Length 357;
Best Local Similarity 81.6%; Pred. No. 6.1e-96;
Matches 253; Conservative 24; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNWVNDSTIOEIIIGFSDRPWLEFPPLVVLISYTVTFGNLTIIIVSRDLTKLHPMY 60
DB 1 MNWVNSVQGEFILLVFSDDQWLEIPFVWMLFYSYILTFGNLTIIIVSHVDFKLHPMY 60
QY 61 FFLNLSLDDCTTCTTCYVPMVLNLCSTIRKVISYGCVAQOLFIFLALGATEYLLAVWSF 120
DB 61 FFLNLSLDDCTTCTTCYVPMVLNLCSTIRKVISYGCVAQOLFIFLALGATEYLLAVWSF 120
QY 121 DMFAICRPLHYSTMORLCLOLAASWVGFNSVWLSITLITOLPLCDYVIDHFCE 180
DB 121 DMFAICRPLHYSTMORLCLOLAASWVGFNSVWLSITLITOLPLCDYVIDHFCE 180
QY 181 VPALLKSCVETANEAELEFVSELFLIPLTLILISYAFIVRAVLRIOSEGRKAFGT 240
DB 181 VPALLKSCVETANEAELEFVSELFLIPLTLILISYAFIVRAVLRIOSEGRKAFGT 240
QY 241 CGSHLIYVSLEYFAYISWYLOPPSPSSKDGKMSLFYGIAPMLNPLIYLRNKEVEG 300
DB 241 CGSHLIYVSLEYFAYISWYLOPPSPSSKDGKMSLFYGIAPMLNPLIYLRNKEVEG 300
QY 301 FKRLVAVFL 310
DB 301 FKRLVAVFL 310

RESULT 3
; Sequence 49, Application US/09907218
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patnrajan, Meera
; APPLICANT: Tallon, Bruce
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam Ryan
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly Ann
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-061
; CURRENT APPLICATION NUMBER: US/09/907, 218
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/218,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/260,977
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/263,801
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/268,226
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/271,622
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-218-49

Query Match 80.8%; Score 1295; DB 5; Length 310;
Best Local Similarity 81.3%; Pred. No. 1.1e-95;
Matches 253; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNWVNDSTIOEIIIGFSDRPWLEFPPLVVLISYTVTFGNLTIIIVSRDLTKLHPMY 60


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Db      1 MNWVNSVPOEFLILVSDPFWLEIPFVWFELSYLTITFGNLTITLIVSHVDRLHTPMY 60
QY      61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
Db      61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
QY      121 DMFVAICRPLHYSVIMHQRICFOLAASWVTSNSVWSTLTITQPLCDPYVIDHFLCE 180
Db      121 DMFVAICRPLHYSVIMHQRICFOLAASWVTSNSVWSTLTITQPLCDPYVIDHFLCE 180
QY      181 VPALLKSCVETANEAELEFVSELFLHILPLTILISYAFIVRAVLRIOSEGRKAFGT 240
Db      181 VPALLKSCVETANEAELEFVSELFLHILPLTILISYAFIVRAVLRIOSEGRKAFGT 240
QY      241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVKEG 300
Db      241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVKEA 300
QY      301 FKRLVARVFL 310
Db      301 FKRLVARVFL 310

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RESULT 4
US-09-965-422-52

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; Sequence 52, Application US/09965422
; GENERAL INFORMATION:
; APPLICANT: Szytek, Kimberly A
; APPLICANT: Casman, Stacie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Dickson, Kevin
; APPLICANT: Vermet, Corine
; APPLICANT: Spaderma, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ediger, Shlomit
; APPLICANT: Macdougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Taylor, Sarah
; APPLICANT: Gunther, Erik
; APPLICANT: Tcheney, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02

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; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-965-422-52

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Query Match 80.6%; Score 1295; DB 5; Length 357;
Best Local Similarity 81.3%; Pred., No. 1.3e-95;
Matches 252; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

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QY      1 MNWVNSIIOEFLILGFSRPMLEFPLLVFLISYTYTIFGNLTITLIVSRDRTKHTPMY 60
Db      1 MNWVNSVPOEFLILVSDPFWLEIPFVWFELSYLTITFGNLTITLIVSHVDRLHTPMY 60
QY      61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
Db      61 FFLTNLSLDLCYTTCTVPMOLVNLCSIRKVISYRGCAOLFIFLAGATEYLLAVMSF 120
QY      121 DMFVAICRPLHYSVIMHQRICFOLAASWVTSNSVWSTLTITQPLCDPYVIDHFLCE 180
Db      121 DMFVAICRPLHYSVIMHQRICFOLAASWVTSNSVWSTLTITQPLCDPYVIDHFLCE 180
QY      181 VPALLKSCVETANEAELEFVSELFLHILPLTILISYAFIVRAVLRIOSEGRKAFGT 240
Db      181 VPALLKSCVETANEAELEFVSELFLHILPLTILISYAFIVRAVLRIOSEGRKAFGT 240
QY      241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVKEG 300
Db      241 CGSHLIIVSLFYSTAVSVYLQPPSPSSKDGKMWSLFYGIAPMLNPLIYTLRNKEVKEA 300
QY      301 FKRLVARVFL 310
Db      301 FKRLVARVFL 310

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RESULT 5

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; US-09-907-218-48
; Sequence 48, Application US/09907218
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patirajan, Meera
; APPLICANT: Tallon, Bruce
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam Ryan
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Szytek, Kimberly Ann
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-061
; CURRENT APPLICATION NUMBER: US/09/907,218
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/218,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/260,977
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/263,801
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/268,226
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/271,622
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-09-907-218-48

Query Match 80.6%; Score 1295; DB 5; Length 357;
Best Local Similarity 81.3%; Pred. No. 1.3e-95;
Matches 252; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNNVNDSTIOEFLILGSDRPMLEFLLVFLSYVTYITFGNTITILVSRDLTKLHMPY 60
DB 1 MNNVNSVPOEFLILVPSDQPMLEIPFVFLFSLYITFGNTITILVSHVDRKLTMPY 60
QY 61 FELTNSLIDLCTTCTTVPQMLVNLCSIRKVIYSGCAQLFTFLAGATEYLLAVMSF 120
DB 61 FELTNSLIDLCTTCTTVPQMLVNLCSIRKVIYSGCAQLFTFLAGATEYLLAVMSF 120
QY 121 DMFVAICRPLHYSVIMHQRCLQLAAASWVGFSNSVWLSLTLLQLPLCDPIYIDHFLCE 180
DB 121 DMFVAICRPLHYSVIMHQRCLQLAAASWVGFSNSVWLSLTLLQLPLCDPIYIDHFLCE 180
QY 181 VPALLKLCVETTANAELEFLVSEFLHPLITLISYAFIVRAVLRIOQAEGRKAFGT 240
DB 181 VPALLKLCVETTANAELEFLVSEFLHPLITLISYAFIVRAVLRIOQAEGRKAFGT 240
QY 241 CGSHLIYVSLFYSTAVSVYIQPPSSSKDQKNVSLFYGIAPMLNPLITLRNKEVKEG 300
DB 241 CGSHLIYVSLFYSTAVSVYIQPPSSSKDQKNVSLFYGIAPMLNPLITLRNKEVKEA 300
QY 301 FKRLVARVFL 310
DB 301 FKRLVARVFL 310

RESULT 6
US-10-032-189-112

; Sequence 112, Application US/10032189
; GENERAL INFORMATION:

; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patturajan, Meera
; APPLICANT: Grose, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard A
; APPLICANT: Grose, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Gorman, Linda
; APPLICANT: Gangoli, Bsha A
; APPLICANT: Rieger, Daniel K
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Gunther, Erik
; APPLICANT: Millet, Isabelle
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-228
; CURRENT APPLICATION NUMBER: US/10/032,189
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 60/257,495
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/258,171
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 60/269,940
; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: 60/274,192
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/277,826
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 60/279,840
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/282,981
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/283,656
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/309,247
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/311,754
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,331
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 112
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-189-112

Query Match 80.6%; Score 1295; DB 6; Length 357;
Best Local Similarity 81.3%; Pred. No. 1.3e-95;
Matches 252; Conservative 25; Mismatches 33; Indels 0; Gaps 0;

QY 1 MNNVNDSTIOEFLILGSDRPMLEFLLVFLSYVTYITFGNTITILVSRDLTKLHMPY 60
DB 1 MNNVNSVPOEFLILVPSDQPMLEIPFVFLFSLYITFGNTITILVSHVDRKLTMPY 60
QY 61 FELTNSLIDLCTTCTTVPQMLVNLCSIRKVIYSGCAQLFTFLAGATEYLLAVMSF 120
DB 61 FELTNSLIDLCTTCTTVPQMLVNLCSIRKVIYSGCAQLFTFLAGATEYLLAVMSF 120
QY 121 DMFVAICRPLHYSVIMHQRCLQLAAASWVGFSNSVWLSLTLLQLPLCDPIYIDHFLCE 180
DB 121 DMFVAICRPLHYSVIMHQRCLQLAAASWVGFSNSVWLSLTLLQLPLCDPIYIDHFLCE 180
QY 181 VPALLKLCVETTANAELEFLVSEFLHPLITLISYAFIVRAVLRIOQAEGRKAFGT 240
DB 181 VPALLKLCVETTANAELEFLVSEFLHPLITLISYAFIVRAVLRIOQAEGRKAFGT 240
QY 241 CGSHLIYVSLFYSTAVSVYIQPPSSSKDQKNVSLFYGIAPMLNPLITLRNKEVKEG 300
DB 241 CGSHLIYVSLFYSTAVSVYIQPPSSSKDQKNVSLFYGIAPMLNPLITLRNKEVKEA 300
QY 301 FKRLVARVFL 310
DB 301 FKRLVARVFL 310

RESULT 7
US-09-965-422-44

; Sequence 44, Application US/09965422
; GENERAL INFORMATION:

; APPLICANT: Spytek, Kimberly A
; APPLICANT: Casman, Stacie
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine
; APPLICANT: Spaderina, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Li, Li
; APPLICANT: Malvanekar, Urial M
; APPLICANT: Taylor, Sarah

```

; APPLICANT: Gunther, Erik
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-965-422-44

```

```

Query Match      78.3%; Score 1259; DB 5; Length 313;
Best Local Similarity 78.0%; Pred. No. 8.3e-93;
Matches 244; Conservative 29; Mismatches 40; Indels 0; Gaps 0;

QY 1 MMWVDSIIQEFILFGSDRPMLEPFLVFLISYVTITFGNLTITLVSRLDTKLTHTPMY 60
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSVANESISREFILFGSDRPMLEPFLVFLISYVTITFGNLTITLVSRLDTKLTHTPMY 60

QY 61 FFLTNLSLDLCYTTCTVPMQMLVNLCSIRKVISYRGCAQOLFPLALGATEYLLAVMSF 120
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 FFLTNLSLDLCYTTCTVPMQMLVNLCSIRKVISYRGCAQOLFPLALGATEYLLAVMSF 120

QY 121 DMFVALICRPLHYSVIMHORCLQLAASWVTGFSNSVMTLTLOLPICDPYVIDHFICE 180
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 DMFVALICRPLHYSVIMHORCLQLAASWVTGFSNSVMTLTLOLPICDPYVIDHFICE 180

QY 181 VPALKLSCVETTANAEELVSEFLHPLITLILSYAFIVRAVLRIOASGRORAFGT 240
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 VPALKLSCVETTANAEELVSEFLHPLITLILSYAFIVRAVLRIOASGRORAFGT 240

QY 241 CGSHLIVSLFSTAVSVYLQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 CGSHLIVSLFSTAVSVYLQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300

QY 301 FKRLVARVFLIKK 313
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 FKRLMKRITLIK 313

RESULT 8
US-09-907-218-45
; Sequence 45, Application US/09907218

```

```

; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Tallon, Bruce
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam Ryan
; APPLICANT: L1, L1
; APPLICANT: Snytek, Kimberly Ann
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-061
; CURRENT APPLICATION NUMBER: US/09/907,218
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/218,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/260,977
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/263,801
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/268,226
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/271,622
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-907-218-45

```

```

Query Match      78.3%; Score 1259; DB 5; Length 313;
Best Local Similarity 78.0%; Pred. No. 8.3e-93;
Matches 244; Conservative 29; Mismatches 40; Indels 0; Gaps 0;

QY 1 MMWVDSIIQEFILFGSDRPMLEPFLVFLISYVTITFGNLTITLVSRLDTKLTHTPMY 60
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 MSVANESISREFILFGSDRPMLEPFLVFLISYVTITFGNLTITLVSRLDTKLTHTPMY 60

QY 61 FFLTNLSLDLCYTTCTVPMQMLVNLCSIRKVISYRGCAQOLFPLALGATEYLLAVMSF 120
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 FFLTNLSLDLCYTTCTVPMQMLVNLCSIRKVISYRGCAQOLFPLALGATEYLLAVMSF 120

QY 121 DMFVALICRPLHYSVIMHORCLQLAASWVTGFSNSVMTLTLOLPICDPYVIDHFICE 180
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 DMFVALICRPLHYSVIMHORCLQLAASWVTGFSNSVMTLTLOLPICDPYVIDHFICE 180

QY 181 VPALKLSCVETTANAEELVSEFLHPLITLILSYAFIVRAVLRIOASGRORAFGT 240
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 VPALKLSCVETTANAEELVSEFLHPLITLILSYAFIVRAVLRIOASGRORAFGT 240

QY 241 CGSHLIVSLFSTAVSVYLQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 CGSHLIVSLFSTAVSVYLQPPSPSSKDGKAVSLFYGIAPMLNPLIYTLNKEVKEG 300

QY 301 FKRLVARVFLIKK 313
   I: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 FKRLMKRITLIK 313

RESULT 9
US-09-907-218-79
; Sequence 79, Application US/09907218
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Tallon, Bruce
; APPLICANT: Casman, Stacie J
; APPLICANT: Wolenc, Adam Ryan
; APPLICANT: L1, L1

```

```

? PRIOR FILING DATE: 2001-07-27
? PRIOR APPLICATION NUMBER: 60/243,497
? PRIOR FILING DATE: 2000-10-26
? PRIOR APPLICATION NUMBER: 60/244,542
? PRIOR FILING DATE: 2000-10-31
? PRIOR APPLICATION NUMBER: 60/269,031
? PRIOR FILING DATE: 2001-02-15
? PRIOR APPLICATION NUMBER: 60/245,484
? PRIOR FILING DATE: 2000-11-03
? PRIOR APPLICATION NUMBER: 60/255,017
? PRIOR FILING DATE: 2000-12-12
? PRIOR APPLICATION NUMBER: 60/263,216
? PRIOR FILING DATE: 2001-01-22
? PRIOR APPLICATION NUMBER: 60/268,225
? PRIOR FILING DATE: 2001-02-12
? NUMBER OF SEQ ID NOS: 209
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 70
? LENGTH: 313
? TYPE: PR1
? ORGANISM: Homo sapiens
US-09-981-566A-70

```

	Query Match	70.38;	Score 1130;	DB 5;	Length 313;
	Best Local Similarity	70.38;	Pred. No. 1.6e-82;		
	Matches 220;	Conservative 34;	Mismatches 59;	Indels 0;	Gaps 0;

```

Db      1  MNWNESSPKKEFLIGFSDRAMLQMPLEFVLLISITITIGNSIMWVCLIDPELTPMY 60
QY      61  FELTNESLLDLCYTCVCPQMWNLCSIRKIVSYRGVQAOLFELALGATEYLLIANMSF 120
Db      61  FELTNESLLDLCYTTTVPPLVNNIGCNKKTISTAGVVAHLILFLAAGATECLLAAMSF 120
QY      121  DMFPAIRPLPHYYSYIMQRLCLQLAASWVTGESNSWMLSTLTQLPCLDPYVIDHFLCE 180
Db      121  DRYAVACRPFLHYVYIMWYMCILPRAASWILGFGNSVLOSSTFLNMPRCHOEVDHFCE 180
QY      181  VPALLKTSCEVTNENAELEFLYSLEFLILPLTLLISYAFIVRAVLVIOGAEGROKAFGT 240
Db      181  VPALLKUSCAQTKPIEELFEFVSLILILIPVTLTLISYGTIAQVAVLIRSAEGROKAFGT 240
QY      241  CGSHLIYVSLFYSYAVSVYLOPPSPSSKDGKNVSLFYGIITAPMLNPLIYTLRNKEYEG 300
Db      241  CGSHMIYVSLFYSGAIYMYLOPPSPSTSKDGKNVSLFYGIITSMNLNLIYSLRNKDKMEA 300
QY      301  FKRLARVFLIHK 313
Db      301  FKRLMPRIFFCKK 313

```

```

RESULT 11
PCT-US02-03635-48
: Sequence 48, Application PC/TUS0203635
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: TRIBOULEY, Catherine M.
: APPLICANT: NGUYEN, Daniel B.
: APPLICANT: THORNTON, Michael
: APPLICANT: YAO, Monique G.
: APPLICANT: KALLICK, Deborah A.
: APPLICANT: GANDHI, Ameera R.
: APPLICANT: WALIA, Narinder K.
: APPLICANT: ARVIZU, Chandra
: APPLICANT: ELLIOTT, Vicki S.
: APPLICANT: HAFALIA, April J.A.
: APPLICANT: RAMKUMAR, Jayalaxmi
: APPLICANT: JIN, Pei
: APPLICANT: TANG, Y.Tom
: APPLICANT: YUE, Henry

```

```

; APPLICANT: REDDY, Roopa
; APPLICANT: BUREFORD, Neil
; APPLICANT: LU, Dyung, Alina M.
; APPLICANT: GRAUL, Richard C.
; APPLICANT: KAHN, Farrah A.
; APPLICANT: WALSH, Roderick T.
; APPLICANT: ISON, Craig H.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: YANG, Junming
; APPLICANT: LEE, Ernestine A.
; APPLICANT: HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/03635
; PRIOR APPLICATION NUMBER: 60/267,322; 60/271,215; 60/274,551; 60/278,507;
; 60/280,597; 60/281,107; 60/282,121
; PRIOR FILING DATE: 2001-02-07; 2001-02-23; 2001-03-08; 2001-03-23;
; 2001-03-30; 2001-04-02; 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc-feature
; OTHER INFORMATION: Incyte ID No: 55019501CD1
PCT-US02-03635-48
```

```

Query Match          58.9%; Score 947; DB 1; Length 318;
Best Local Similarity 59.7%; Pred. No. 6,7e-68;
Matches 178; Conservative 49; Mismatches 71; Indels 0; Gaps 0;

QY 10 QETILIGSDRPMLEPPLVPLVLIISTVTITFGNLTIIIVSRDLTKHTMYFFLNLSSL 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 14 KPEILIGISRPWLEPFAVLVLYFLMLGNISIIIVSQDLDPQHSPIYIFLSHLSFL 73
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 DLCYTCVPMVNCSTRKIVSYRGCAQLFIPLALGATEVLLAVMSFDMFVAICRP 129
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 74 DLTCTTTTVPOMLFNMGSSCKTISYGGCTVOVAIFMVLGTECVLAAMLDRAVALCEP 133
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 130 LHYVIMHORLCLOLAASWVTGFSNSVWLSTLTLOPLCDPYVIDHFLCEVPALLKLSL 189
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 134 LRAIILIMHRLCOQLVAMAMLSGFGNSLVQVILTVQLPFCGRQVANNFCEVPAVAMIKLSL 193
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 190 VETANEAEFLVSELPHILPTLLIISAFIVRAVLRIQASGRKAKGTGSHLIIVS 249
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 194 ADPTANDATLAVLVAFVFLVPLLLILISYGFIRAVWRIOSSGRHKAFTGSSHLIIVS 253
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 250 LEVSTAVSVYLOPPSSSKDOGMVSLFVGIIAPMLNPLIYTLRNKEVEGFRVLVAR 307
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 254 LFLPALIYMLOPPSSYSOEGKFTISLFTSIITPLNPTTYTLRNKDKGALRLRLAR 311
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```

RESULT 12
; US-09-546-986A-2
; Sequence 2, Application US/09546986A
; GENERAL INFORMATION:
; APPLICANT: Powers, Scott
; APPLICANT: Yang, Jianxin
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: Novel G-Protein Coupled Receptors
; FILE REFERENCE: 018781-00472005
; CURRENT APPLICATION NUMBER: US/09/546,986A
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 09/524,730
; PRIOR FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 16
```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-546-986A-2
```

```

Query Match          58.4%; Score 939; DB 5; Length 310;
Best Local Similarity 58.7%; Pred. No. 2.8e-67;
Matches 175; Conservative 50; Mismatches 73; Indels 0; Gaps 0;

QY 12 FILLGSDRPMLEPPLVPLVLIISTVTITFGNLTIIIVSRDLTKHTMYFFLNLSSL 71
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 9 FILLGSDRPMLEPPLVPLVLIISTVTITFGNLTIIIVSRDLTKHTMYFFLNLSSL 68
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 CYTTCVPMVNCSTRKIVSYRGCAQLFIPLALGATEVLLAVMSFDMFVAICRP 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 CYTTCVPMVNCSTRKIVSYRGCAQLFIPLALGATEVLLAVMSFDMFVAICRP 128
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 YSVIMHORLCLOLAASWVTGFSNSVWLSTLTLOPLCDPYVIDHFLCEVPALLKLSL 191
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 YAVIMHRLCOQLVAMAMLSGFGNSLVQVILTVQLPFCGRQVANNFCEVPAVAMIKLSL 188
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 TTANEAEFLVSELPHILPTLLIISAFIVRAVLRIQASGRKAKGTGSHLIIVS 251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 TANDATLAVLVAFVFLVPLLLILISYGFIRAVWRIOSSGRHKAFTGSSHLIIVS 248
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 252 YSTAVSVYLOPPSSSKDOGMVSLFVGIIAPMLNPLIYTLRNKEVEGFRVLVAR 309
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 249 YLPAIYMLOPPSSYSOEGKFTISLFTSIITPLNPTTYTLRNKDKGALRLRLAR 306
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RESULT 13
PCT-US02-03635-32
; Sequence 32, Application PC/TUS0203635
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: THORNTON, Michael
; APPLICANT: YAO, Monique G.
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Narendra K.
; APPLICANT: ARVIZU, Chandra
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: RAMKOMAR, Jayalaxmi
; APPLICANT: JIN, Pei
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: REDDY, Roopa
; APPLICANT: BUREFORD, Neil
; APPLICANT: LU, Dyung, Alina M.
; APPLICANT: GRAUL, Richard C.
; APPLICANT: KAHN, Farrah A.
; APPLICANT: WALSH, Roderick T.
; APPLICANT: ISON, Craig H.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: YANG, Junming
; APPLICANT: LEE, Ernestine A.
; APPLICANT: HARLAND, Lee
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0357 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/03635
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/267,322; 60/271,215; 60/274,551; 60/278,507;
; 60/280,597; 60/281,107; 60/282,121
; PRIOR FILING DATE: 2001-02-07; 2001-02-23; 2001-03-08; 2001-03-23;
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; 2001-03-30; 2001-04-02; 2001-04-06
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PERL Program
; SEQ ID NO 32
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7477359CD1
PCT-US02-03635-32

Query Match      58.2%; Score 936; DB 1; Length 309;
Best Local Similarity 59.3%; Pred. No. 4.9e-67;
Matches 179; Conservative 51; Mismatches 72; Indels 0; Gaps 0;

QY 5 NDSIIIOEFLIGFSRDMLEFPLLVFLISYTVTIFGNLTIIIVSRDLTGHMPYFELT 64
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 NDSIIMDFILIGFSRDMLEFPLLVFLISYTVTIFGNLTIIIVSRDLTGHMPYFELS 64
QY 65 NLSLIDLCYTTCTVPQMLVNLCSIRKVISYRGCAOQLFIFLAGATEYLLAVMSFDMFV 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 NLSLIDLCFTTSLAPQVLVNLQRPKRTITVGGCAOQLYISLAGSTECILLADMDRYI 124
QY 125 AICRPLHYSTMHORLCLQAAASWTFGSNSWLSLTITQLPLCDPYVIDHFLCEVPAL 184
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 AVCKPLHYVIMNPRICQOQLASISWLSGLASSLIHAFITQLPLCGNHRDLHFICEVPAL 184
QY 185 LKLSCEVTANEAELFVLSLFLHPLITLLISYAFIVRAVLRQSAEGROKAFGTCGSH 244
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 LKLAQVDITVNLVLFVSVLFPVITPALISISYGFITQAVLRKISYEARRHKAFTSCSSH 244
QY 245 LTVVSLFYSTAVSVYIOLPPSPSSKDGKMYSLFYGIAPMLNPLITYLRNKEVKEGFKRL 304
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 245 LTVVLIIFYGTIIYVYIOLPPSDSYADQCKFISLFTVWTPPLNPIITYLRNKKMEALRKL 304
QY 305 VA 306
Db 305 LS 306

RESULT 14
US-09-965-422-12
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Casman, Stacie
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Dickson, Kevin
; APPLICANT: Vernet, Corine
; APPLICANT: Spaderina, Steven K
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Gerlach, Valerie
; APPLICANT: Ellerman, Karen
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John R
; APPLICANT: Smithson, Glenda
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Urulal M
; APPLICANT: Taylor, Sarah
; APPLICANT: Gunther, Erik
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21401-132
; CURRENT APPLICATION NUMBER: US/09/965,422
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,286
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/236,284
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/237,581
; PRIOR FILING DATE: 2000-10-03
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; PRIOR APPLICATION NUMBER: 60/238,735
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/240,736
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/260,019
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,338
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/262,156
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/262,498
; PRIOR FILING DATE: 2001-01-18
; PRIOR APPLICATION NUMBER: 60/263,133
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,691
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/266,109
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/271,634
; PRIOR FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-965-422-12

Query Match      58.2%; Score 936; DB 5; Length 309;
Best Local Similarity 59.3%; Pred. No. 4.9e-67;
Matches 179; Conservative 51; Mismatches 72; Indels 0; Gaps 0;

QY 5 NDSIIIOEFLIGFSRDMLEFPLLVFLISYTVTIFGNLTIIIVSRDLTGHMPYFELT 64
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Db 5 NDSIIMDFILIGFSRDMLEFPLLVFLISYTVTIFGNLTIIIVSRDLTGHMPYFELS 64
QY 65 NLSLIDLCYTTCTVPQMLVNLCSIRKVISYRGCAOQLFIFLAGATEYLLAVMSFDMFV 124
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 65 NLSLIDLCFTTSLAPQVLVNLQRPKRTITVGGCAOQLYISLAGSTECILLADMDRYI 124
QY 125 AICRPLHYSTMHORLCLQAAASWTFGSNSWLSLTITQLPLCDPYVIDHFLCEVPAL 184
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 AVCKPLHYVIMNPRICQOQLASISWLSGLASSLIHAFITQLPLCGNHRDLHFICEVPAL 184
QY 185 LKLSCEVTANEAELFVLSLFLHPLITLLISYAFIVRAVLRQSAEGROKAFGTCGSH 244
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 185 LKLAQVDITVNLVLFVSVLFPVITPALISISYGFITQAVLRKISYEARRHKAFTSCSSH 244
QY 245 LTVVSLFYSTAVSVYIOLPPSPSSKDGKMYSLFYGIAPMLNPLITYLRNKEVKEGFKRL 304
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Db 245 LTVVLIIFYGTIIYVYIOLPPSDSYADQCKFISLFTVWTPPLNPIITYLRNKKMEALRKL 304
QY 305 VA 306
Db 305 LS 306

RESULT 15
US-10-032-189-111
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Patlurajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shinkets, Richard A
; APPLICANT: Grosse, William M
```

```

: APPLICANT: Szekeres, Edward S
: APPLICANT: Vermet, Corine A.M.
: APPLICANT: Li, Li
: APPLICANT: Casman, Stacie J
: APPLICANT: Boldog, Ferenc L
: APPLICANT: Gorman, Linda
: APPLICANT: Gangoll, Eshe A
: APPLICANT: Fernandes, Elma R
: APPLICANT: Rieger, Daniel K
: APPLICANT: Edinger, Shlomit R
: APPLICANT: Gunther, Erik
: APPLICANT: Millet, Isabelle
: APPLICANT: Sciore, Paul
: APPLICANT: Ellerman, Karen
: APPLICANT: MacDougall, John R
: APPLICANT: Smithson, Glenda
: TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
: FILE REFERENCE: 21402-228
: CURRENT APPLICATION NUMBER: US/10/032,189
: CURRENT FILING DATE: 2001-12-21
: PRIOR APPLICATION NUMBER: 60/257,495
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/258,171
: PRIOR FILING DATE: 2000-12-20
: PRIOR APPLICATION NUMBER: 60/269,940
: PRIOR FILING DATE: 2001-02-20
: PRIOR APPLICATION NUMBER: 60/274,192
: PRIOR FILING DATE: 2001-03-08
: PRIOR APPLICATION NUMBER: 60/277,826
: PRIOR FILING DATE: 2001-03-22
: PRIOR APPLICATION NUMBER: 60/279,840
: PRIOR FILING DATE: 2001-03-29
: PRIOR APPLICATION NUMBER: 60/282,981
: PRIOR FILING DATE: 2001-04-11
: PRIOR APPLICATION NUMBER: 60/283,656
: PRIOR FILING DATE: 2001-04-13
: PRIOR APPLICATION NUMBER: 60/309,247
: PRIOR FILING DATE: 2001-07-31
: PRIOR APPLICATION NUMBER: 60/311,754
: PRIOR FILING DATE: 2001-08-17
: PRIOR APPLICATION NUMBER: 60/313,331
: PRIOR FILING DATE: 2001-08-17
: NUMBER OF SEQ ID NOS: 260
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 111
: LENGTH: 309
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-032-189-111

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Query Match          58.2%; Score 936; DB 6; Length 309;
Best Local Similarity 59.3%; Pred. No. 4.9e-67;
Matches 179; Conservative 51; Mismatches 72; Indels 0; Gaps 0;

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QY 5 NDSIIQEFILIGSDRWLEFPLLYVFLISYTYIIFGNLTIIIVSRDITKLTHTPMYFFLT 64
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| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 65 NLSLDDCTTTCVPOMLVNCISIRKVISRGCAOLFPLALGATEYLLAVSPDMFV 124
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 65 NLSLDDCTTTCVPOMLVNCISIRKVISRGCAOLFPLALGATEYLLAVSPDMFV 124
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QY 125 AICRPLHYVIMHQRLCLQIAASWYTGFSNYSWLSTLTQLPLCDPYVIDHFLCEVPAL 184
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QY 185 LKISCVEETANEAEPLVSELPFHLIPTLLISYAFIVRAVLRQSAEGROKAGTCGSH 244
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
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Db 245 LTVVLIIFYGITIIYVYLOPSPDSYADOGKFIISLFTYMTPTILNPITITLRNKDKKALRL 304
QY 305 VA 306
Db 305 LS 306

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Search completed: August 25, 2002, 20:15:19
Job time: 482 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 14:56:02 ; Search time 1869.44 Seconds

(without alignments)
10555.955 Million cell updates/sec

Title: US-09-800-321A-3

Perfect score: 943
Sequence: 1 tatgaattgggttaaatgaca.....tcttcttaatcaagaataa 943

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb.ba:*
2: gb.hg:*
3: gb.in:*
4: gb.om:*
5: gb.ov:*
6: gb.pat:*
7: gb.ph:*
8: gb.pl:*
9: gb.pr:*
10: gb.ro:*
11: gb.sts:*
12: gb.sy:*
13: gb.un:*
14: gb.vl:*
15: em.ba:*
16: em.fun:*
17: em.hum:*
18: em.in:*
19: em.mu:*
20: em.om:*
21: em.or:*
22: em.ov:*
23: em.pat:*
24: em.ph:*
25: em.pl:*
26: em.ro:*
27: em.sts:*
28: em.un:*
29: em.vl:*
30: em.hg.hum:*
31: em.hg.inv:*
32: em.hg.other:*
33: em.hggo.inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query #
No. score Match Length DB ID Description

1	943	100.0	943	6	AX282353	Sequence
2	940.4	99.7	993	6	AX282351	Sequence
3	940.4	99.7	44788	6	AL133267	Human DNA
4	940.4	99.7	176277	2	AC025941	Human DNA
5	938.8	99.6	942	6	AX195281	Sequence
6	938.8	99.6	1488	6	AX195283	Sequence
7	937.4	99.4	939	6	AX241843	Sequence
8	937.2	99.4	956	6	AX282355	Sequence
9	727.8	77.2	1074	6	AX241494	Sequence
10	726.2	77.0	1071	6	AX241494	Sequence
11	726.2	77.0	1071	6	AX242075	Sequence
12	726.2	77.0	1074	9	HS302584	Sequence
13	726.2	77.0	1074	9	HS302585	Sequence
14	726.2	77.0	1074	9	HS302586	Sequence
15	726.2	77.0	1074	9	HS302587	Sequence
16	726.2	77.0	1074	9	HS302588	Sequence
17	726.2	77.0	1074	9	HS302589	Sequence
18	726.2	77.0	1074	9	HS302590	Sequence
19	726.2	77.0	1074	9	HS302591	Sequence
20	726.2	77.0	1074	9	HS302592	Sequence
21	726.2	77.0	100375	9	HS193812	Sequence
22	726.2	77.0	166758	2	AC024428	Sequence
23	726.2	77.0	176277	2	AC025941	Sequence
24	666.8	70.7	942	10	AY073555	Sequence
25	665.2	70.5	185331	2	AL589742	Sequence
26	647.4	68.7	649	9	U86270	Sequence
27	647.4	68.0	648	6	AX242056	Sequence
28	630.6	66.9	648	9	U86271	Sequence
29	610.2	64.7	646	9	U86275	Sequence
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31	602.8	63.9	942	10	AY073554	Sequence
32	600.6	63.7	161043	10	AL589651	Sequence
33	590.4	62.6	940	10	AY074039	Sequence
34	588.4	62.4	1214	10	RATOLIRECE	Sequence
35	535.6	56.8	942	9	HS302546	Sequence
36	534	56.6	942	9	HS302537	Sequence
37	534	56.6	942	9	HS302538	Sequence
38	534	56.6	942	9	HS302539	Sequence
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40	534	56.6	942	9	HS302541	Sequence
41	534	56.6	942	9	HS302542	Sequence
42	534	56.6	942	9	HS302543	Sequence
43	534	56.6	942	9	HS302544	Sequence
44	534	56.6	942	9	HS302545	Sequence
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ALIGNMENTS

RESULT 1
AX282353
LOCUS AX282353 943 bp DNA
DEFINITION Sequence 3 from Patent WO0166746.
ACCESSION AX282353
VERSION AX282353.1 GI:16609543
KEYWORDS
SOURCE
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Padigaru,M., Burgess,C.E., Majumder,K., Mishra,V.S., Li,L.,
Baumgartner,J.C., Spytek,K.A. and Tchernev,V.T.
TITLE G-protein coupled receptor related polypeptides
JOURNAL Patent: WO 0166746-A 3 13-SEP-2001,
Curagen Corporation (US)
FEATURES
source Location/Qualifiers
1. 943
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 221 a 227 c 187 g 308 t
ORIGIN

Query Match 100.0%; Score 943; DB 6; Length 943;
Best Local Similarity 100.0%; Pred. No. 2.4e-257;
Matches 943; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 tatgaattggtaataagacagcatcacaagaggttatctctggtggttcctcagatcg 60
    |||||||
DB 1 TATGAATTGGTAAATGACAGCATACAGAGGATTTATCTCTGGGTTTCAGATCG 60
QY 61 acctggctggaggttccacctcttggtctctcttgattcttaccctgtgacatctt 120
    |||||||
DB 61 ACCTTGGCTGGAGTTTCCACTCTTGTTGGCTCTCTTGATTCTTACACTGTGACATCTT 120
QY 121 tggcaactctgacatattctctagtgcaagcctctgacacacaaactcacaaccccatgta 180
    |||||||
DB 121 TGGCAATCTGACATATTCTAGTGTACAGCCCTGGAACCAACTTCATACCCCATGTA 180
QY 181 ttttttcttacaatcatcatcactcctctgagatctctgtttacacacatgtacagtcacaa 240
    |||||||
DB 181 TTTTTCCTTACCAATCATCACTCCTGATCTTGTTCACCAATGTACAGTCCACACA 240
QY 241 aatgctagaataatttatgacagcatcaggaagaatcaagttacgttgcgtgtgtagccca 300
    |||||||
DB 241 AATGCTAGTAATTTATGACAGCATCAGAGAAATGATCAGTTATGAGCTGTAGGCCA 300
QY 301 gctttcacaattctctgaccttgggggctactgataatctctcctgtgacgtcgtcctt 360
    |||||||
DB 301 GCTTTTCATATTTCTGGCCCTGGGGGCTACTGAAATCTTCTCTGGCCGCTCATGTCTT 360
QY 361 tgatttggtttagtactattgtgcgacctcacttactcagttacatcaatgacagagact 420
    |||||||
DB 361 TGAATTTGGTTTGTAGCATTTGTGTGGCCCTCCATCTACTCAGTTATCATGACACAGAGACT 420
QY 421 ctgcccacagttggagcctgacatccctgggttactggttttagtaactcagttggtgttc 480
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DB 421 CTGCCCTCAGATTTGGAGCTGATCCTGGGTTACTGGTTTATGATCTCAGTGTGTTGTC 480
QY 481 taacctgaactctcagcctgacatctgtgacacctatgtatagatcaacttctctgtga 540
    |||||||
DB 481 TACCTGAGACTCTCAGCTGACATCTGTGACCCCTATGTATGATCATTCTCTGTGA 540
QY 541 agtccctgacatctgactaagtatctgtgtgtgagacaaagagaaatgagagctgaactatt 600
    |||||||
DB 541 AGTCCTGACACTGCTCAAGTTATCTTGTGTGAGACAAAGCAAGAGCTGAACTATT 600
QY 601 ccttgcaatgagctcttccatcttaataacccctgacacatcatccttatatcatgtctt 660
    |||||||
DB 601 CCTTGACAGAGACTCTTCCATCTTAATACCCCTGACACATCATCTTATATCATATGCTTT 660
QY 661 taattgcgagagatattgagatatacagctctgtaaggtcgacaaaagaacatttggagac 720
    |||||||
DB 661 TATTTGCCGAGAGATTTGAGATFACAGTCTGTGAAGGTCGACAAAAGCATTTGGGAC 720
QY 721 atgtgttccacataatgtgtgtgtctctttttatagtaagcagcgtctctgtgaacct 780
    |||||||
DB 721 ATGTGTTCCACTTAATGTGTGTGTCTTTTATATGACAGCCGTCTGTGTGACCT 780
QY 781 gcaaacacattcgcccaagctcacaagaaagaaagatgttctctcttctcattgaat 840
    |||||||
DB 781 GCNAACACCTTGCCCAAGCTCCAAAGGCAAGAAAGATGTTCTCTCTATGGAAT 840
QY 841 catgtacacacatgtcgaatcccttatatacacttaggaacaagaggttaagaagag 900
    |||||||
DB 841 CATTTGACCCATGCTCAATCCCTTATATATACACTTAGAACAAAGAGAGTAAAGGAAG 900
QY 901 ctttaaaaggttggtgcaagagctctcttaacaaagaaataa 943
    |||||||
DB 901 CTTTAAAGGTGTGTGCAAGAGTCTTCTTAATCAAGAAATAA 943
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RESULT 2
AX282351

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LOCUS AX282351 993 bp DNA linear PAT 02-NOV-2001
DEFINITION Sequence 1 from Patent WO0166746.
ACCESSION AX282351
VERSION AX282351.1 GI:16609542
KEYWORDS
SOURCE
ORGANISM human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (sites)
AUTHORS Padigar,M., Burgess,C.E., Majumder,K., Mishra,V.S., Li,L.,
Baumgartner,J.C., Spytek,K.A. and Tchernev,Y.T.
TITLE G-protein coupled receptor related polypeptides
JOURNAL Patent: WO 0166746-A 1 13-SEP-2001;
        Curen Corporation (US)
FEATURES
    source             1..993
                        Location/Qualifiers
BASE COUNT 246 a 233 c 194 g 320 t
ORIGIN
Query Match 99.7%; Score 940.4; DB 6; Length 993;
Best Local Similarity 99.9%; Pred. No. 1.3e-256;
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OY	782	caaccaccttcgccagtccaaaggacaaggaaaagaatgtgttctctcttctatgaatc	841
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DESCRIPTION	Human DNA sequence from clone RPJ-408B20 on chromosome 6. Contains a gene and two pseudogenes for 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) proteins and a gene for a novel protein similar to 60S acidic ribosomal protein P2 (RPLP2), ESTs, SMS and GSSs, complete sequence.		
ACCESSION	AL133267		
VERSION	AL133267.9 GI:10185396		
KEYWORDS	HNG; 7 transmembrane; olfactory receptor; ribosomal protein; RPLP2.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 (bases 1 to 44788)		
JOURNAL	Williams, S.		
COMMENT	Direct Submission Submitted (20-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Requests: clonerequests@sanger.ac.uk On Sep 18, 2000 this sequence version replaced gi:9588470. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences without only a small overlap as described above. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; SW:, SWISSPROT; Tr:, TREMBL; Wp:, WormPEP; Information on the WormPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/WormPEP This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 IMPORTANT: This sequence is not the entire insert of clone RPJ-408B20 it may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RPJ-3116 is at 44689 in this sequence. The true right end of clone RPJ-193812 is at 100 in this sequence. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPJ-408B20 is from the library RPJ-C3 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pCPYPAC2.		

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SEQUENCE, 15 unordered pieces.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 6, clone RP11-635011
Unpublished
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
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Young, G., Zahoun, J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 4, 2000 this sequence version replaced g1:7259782.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L8577
Center clone name: 635_O_11
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Chemistry: Dye-terminator Big Dye 100% of reads
Assembly program: Phrap; version 0.960731
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Insert size: 176000: agarose-fp
Insert size: 174877: sum-of-contigs
Quality coverage: 4.5 in Q20 bases; agarose-fp
Quality coverage: 4.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
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2998 3097: gap of 100 bp
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Matches 941; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 153754 TGCCTCAGTTTGCAGGTGATCTCTGGGTACAGTTTATAGTAAGTGTGTGTCT 153695

QY 482 accctgaacctcgaagctgacacctctgtgacccctatgtatagatcaactcttcctgtga 541
DB 153694 ACCCTGACCTCCAGCTGACACCTGTGACCCCTATGTGATGATCACTTCTCTGTGA 153635

QY 542 gtccctgaactgtcgaagtatctgtgtgagaacaacaagaatgagctgaactatc 601
DB 153634 GTCCCTGCACTGCTCAAGTTATCTTGTGTGAGACACAAATGAGCTGACTATTC 153575

QY 602 ctgttcagtgagctcttccaactcaatccctgacacatccctatcatcatactgtctt 661
DB 153574 CTGTGAGTGAGCTCTTCCATTAATACCCCTGACACTCATCTTATATCATATGCTTT 153515

QY 662 atgtctcagagcaglatatgagatacagctctgtcgaaggtcgcacaaaagcatltyggaca 721
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QY 722 tgtgtgtcccaatcaatctgtgtgtctcttcttataagtaacgctctctgtgtacctg 781
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QY 782 caaccacactcgcgcagctcccaagaaccaagaagaatggttctctctctctctatcgtgaac 841
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QY 842 attgcaaccaatgtcgaatccctctatataatacaactagaagaagaaggtlaaagaagc 901
DB 153334 ATTGCAACCATGCTGAATCCCTTATATATACACTTAGGAACAAGAGGTAAAGGAAGGC 153275

QY 902 ttttaaaaggttggltgcaagaagctcttctaataaagaataa 943
DB 153274 TTTAAAGGTGGTGCAGAGTCTTCTTAATCAAGAAATAA 153233

RESULT 5
AX195281 AX195281 942 bp DNA linear PAT 28-AUG-2001
LOCUS

DEFINITION Sequence 1 from Patent WO0151634.
ACCESSION AX195281
VERSION AX195281.1 GI:15385832
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 942)
AUTHORS Walke,D.W., Milgromski,N.L., Turner,C.A., Friedrich,G., Abuln,A., Zambrowicz,B. and Sands,A.T.
TITLE Human olfactory receptor and polynucleotides encoding the same
JOURNAL Patent: WO 0151634-A 1 19-JUL-2001;
FEATURES
source location/Qualifiers
1. 942
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 222 a 228 c 187 g 305 t
ORIGIN

Query Match 99.6%; Score 938.8; DB 6; Length 942;
Best Local Similarity 99.8%; Pred. No. 3.7e-256;
Matches 940; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 atgaattgggtaaatgacagacatcatcagaagattatcttctgctgggtcttcagaatcga 61
DB 1 ATGAATTGGGTAATATGACACATCATCAGAGATTATTTGCTGGGTTCTCAGATCGA 60

QY 62 ccttgctggaggttcccaacctctgtgtctcttctgaattcttctacactgtgacacattt 121
DB 61 CTTGGCTGGAGTTTCCACCTCTTGCTTCTTGTGATTTCTTACACTGTGACCATCTT 120

QY 122 ggaacatcgacatctatcttaagtgcacggctggaacccaactcaatccccatgtat 181
DB 121 GGCATCTGCACATTAATTTAGTGTACGCGCTGACACCAAACTTCATACCCCATGTAT 180

QY 182 tttttcttccaactatcatctactccctggaactcttctgttacaaccaatgataagtcacca 241
DB 181 TTTTCTTACCATCATCTATCATCTCTGGATCTTGTATACACCATGTACAGTCCACAA 240

QY 242 atgtctagtaaatcatgacagacatcagaagaatcatcagttatctgtgctgtgacccag 301
DB 241 ATGCTAGTAATATTATGACACATCAGAAAGTATATGATTGCTGTGTGTAGCCAG 300

QY 302 ctctcaatattctggccttgggggctgactgaatctctctctggcgcgtcatgtccctt 361
DB 301 CTTTCATATTCTTGCGCTTGGGGGCTACTGAATATCTTCTCTGGCGCTGATGCTCTT 360

QY 362 gatgtgttgaactatcttggcgcctctccatctactcagttatcagtcacagagactc 421
DB 361 GATAGTGTGATCTTGTGCGCTTGGCGCTTCCATTAATCACTATGACACAGAGACTC 420

QY 422 tgcctcagtttgcagctgacatccctgtgttactggttttagtaacccaagtggtgtct 481
DB 421 TGCCTCAGTTTGCACCGCATCTGTGGTTACGTTTAAAGTAATCAAGTGTGTGTCT 480

QY 482 accctgaacctcgaagctgacacctctgtgacccctatgtatagatacaactctctgtga 541
DB 481 ACCCTGACCTCCAGCTGCACTCTGTGACCCCTATGTATGATCACTTCTCTGTGA 540

QY 542 gtccctgaactgtcgaagtatctgtgtgagaacaagaacaaatgagctgtaactatc 601
DB 541 GTCCCTGCACTGCTCAAGTTATCTTGTGTGAGACAAAGCAAAATGAGGCTGAATATTC 600

QY 602 ctgtcagtgagctcttccaactaataacccctgaacatctctatcatcatgtcttct 661
DB 601 CTGTGAGTGAGCTCTTCCATTAATACCCCTGACACTCATCTTATATCATATGCTTTT 660

QY 662 atgtctcagagcaglatatgagatacagctctgtcgaaggtcgcacaaaagcatltyggaca 721
DB 661 ATGTGCGAGCACTATTGAGGATACAGTCTGTGAAGGTGACAAAAGCATTTGGGACA 720

QY 722 tctgttcccatctaatgtgtgtctctctttatagtaagccgctctctgtactg 781
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Db 721 TGTGTTCCCATCTTAATGTGTGTCCTTTTATATAGTACAGCGTCTGTGATCCG 780
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QY 842 atgcaccatctgtaatccctctatatatacacttaagaacaagaagtaagaagc 901
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QY 902 tttaaaaggtgtgttgcgaagctctcttctaacaagaataa 943
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Db 901 TTTAAAGGTTGTTGCAAGAGCTCTCTTATCAAGAATAA 942
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RESULT 6
AX195283 1488 bp DNA linear PAT 28-AUG-2001
LOCUS AX195283 Sequence 3 from Patent WO0151634.
DEFINITION AX195283
ACCESSION AX195283
VERSION AX195283.1 GI:15385833
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1488)
AUTHORS Walke,D.W., Wilganowski,N.L., Turner,C.A., Friedrich,G., Abuin,A.,
Zambowicz,B. and Sands,A.T.
TITLE Human olfactory receptor and polynucleotides encoding the same
JOURNAL Patent: WO 0151634-A 3 19-JUL-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source 1.1488
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 421 a 333 c 254 g 477 t 3 others
ORIGIN
Query Match 99.6%; Score 938.8; DB 6; Length 1488;
Best Local Similarity 99.8%; Pred. No. 3.8e-256;
Matches 940; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 atgaattggtaaatgacagcatcatagaggaattatctgctggtgtctcagatcga 61
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Db 198 ATGAATGGTAATGACAGCATCATACAGAGATTATTCCTGCGTTTCTCAGATCGA 257
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QY 62 ccttggtggaattccaactctgtgtgtctcttgatcttaactctgacatctt 121
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Db 258 CCTTGCGTGGAGTTCCACTCTGTGTGTCCTTGATTTCTTACACGTGACCATCTTT 317
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QY 122 ggcacatcgaccattatctagtgtcagctgagacaaacttacaacccatgat 181
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Db 318 GGCATCTGACCATTTATCTAGTGTGACGCGCTGACACCAACTTCATACCCCATGTAT 377
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QY 182 ttttcttacaactctacactcctgagatctgttaccacacatgacagctccaca 241
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Db 378 TTTTTCCTTACCAATCTATCACTCTGTGATCTTTGTACACCAATGTACAGTCCACAA 437
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QY 242 atgctagtaaatcatcagacatcagaagaatcaatcagtaactgtgctgtgtagccag 301
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Db 438 ATGCTAGTAATTTATGACGATCAGGAAGTAATCACTTATCGGCTGTGAGCCAG 497
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QY 302 ctcttcattctgctgcttggggcttactgaataatcttccctggccgtatgctctt 361
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Db 498 CTTTTCATATTTCTG6CCTTG6G6GCTACTGAAATATCTTCTG6G6GCTATGTCCTTT 557
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QY 362 gattgtttgtagctattgtcgcgctctcatattacattacatcacagaagatc 421
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Db 558 GATAGTTTGTAGCATTTTGTGCGGCTCTCCATTAATCTAGTTATCATGCACAGACTC 617
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QY 422 tgcctcagattgagcagctgcatacctggtgtactggttttagtaactcagtggtgtct 481
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Db 618 TGCCCTCAGTTGGAGCGCGCATCCGTTGTTACTGGTTTATGTAATCTAGTGAGTGCT 677
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QY 482 accctgaactctccagctgcacactgtgtgaacccatgtgataatgaatcttctgtgaa 541
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Db 678 ACCCTGACTCTCCAGCTCCACTGTGTACCCCATGTGAATGATACATTTCTGTGAA 737
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QY 542 gtccctgacagctcaagtatctgtgtgttagaacaagaagaatgagcgaactatc 601
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QY 602 ctgtcagtgagctcttccatataataaccctggaacatcactatatacatatgcttt 661
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Db 858 ATTGTCCAGCAGATATTGAGATACAGTCTGCTGAAGCTGCACAAAAGCATTTGGGACA 917
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QY 722 tctgttcccatctaatgtgtgtctcttttataagtagcagccgtctctgtactg 781
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Db 1098 TTTAAAGGTTGTTGCAAGAGCTCTCTTATCAAGAATAA 1139
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RESULT 7
AX241843 939 bp DNA linear PAT 26-SEP-2001
LOCUS AX241843 Sequence 591 from Patent WO0127158.
DEFINITION AX241843
ACCESSION AX241843
VERSION AX241843.1 GI:15798718
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 939)
AUTHORS Bellenson,J., Smith,D., Lancet,D., Glusman,G., Fuchs,T. and Yanai,I.
TITLE Olfactory receptor sequences
JOURNAL Patent: WO 0127158-A 591 19-APR-2001;
Dgdiscents (US) : YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
FEATURES
source 1.939
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="(H38g440 nucleotide)"
BASE COUNT 220 a 227 c 187 g 305 t
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Query Match 99.4%; Score 937.4; DB 6; Length 939;
Best Local Similarity 99.9%; Pred. No. 9.4e-256;
Matches 938; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 atgaattggtaaatgacagcatcatagaggaattatctgctggtgtctcagatcga 61
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Db 1 ATGAATGGTAATGACAGCATCATACAGAGATTATTCCTGCGTTTCTCAGATCGA 60
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QY 62 ccttgctgaggttccaactcctgtgtgtctcttgattcttaacatcgtgacatctt 121
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Qy ggcacatcgacatattatctagtgtaacagcctgagacacacacacacacacacatgat 181
Db 122 GGCATATCGACATATTATCTAGTGTACAGCTGACACCAACTTTCATACCCCATGTAT 180
Qy 182 tttttcttaacaaactatcaactcctcgatcttcttaccacacacacacacacacaa 241
Db 181 TTTTCTTACCAATCTATCACTCCTGGATCTTGTATACACACATGATGACGTCACAA 240
Qy 242 atgtagtaaatatgatgacagatcaagaaagaaatcaagttatctgtgtgtgtgtgtgt 301
Db 241 ATGTGATGAAATTTATGACGATCAGAGAAATATCAATTCATGCTGTGTGTGTGTGT 300
Qy 302 ctttcataattctgcgcttgggggctactaataatctctcccgccgctgatatctctt 361
Db 301 CTTTTCATATTTTCGGCTTGGGGGCTACATCATCTCTCCGCGCGCTATGTCTTT 360
Qy 362 gattggtttagatattgtcggcctctccataactcaatgacatgacacagagactc 421
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Qy 422 tgcctcaagttgagctgacatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 481
Db 421 TGCTTCAGTTGGAGCTGACATCTGTGGTTACTGTTTAACTGATCACTGATGTGTCT 480
Qy 482 accctgactctcagctgcgacactctgtgacccctatgtagatgactctctctgtgaa 541
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Qy 542 gtccctgactgctcaagttatcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 601
Db 541 GTCCCTGACACTGCTCAAGTTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
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Db 661 ATGTCCGAGAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGATAT 720
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Qy 782 caaccactctgcgacacactcgaagacgaagaaagatgttctctctctctctctctct 841
Db 781 CAACCACTCTGCGCCAGCTCCAAAGACCAAGAAAGATGTGTCTCTCTCTATGGAATC 840
Qy 842 atgtcaccaatgctgaatccctctatatatacacttaggaacaggaaggtaaagaaagc 901
Db 841 ATGTCCAGCAGATATGAGATATGAGATATGAGATATGAGATATGAGATATGAGATAT 900
Qy 902 ttttaaaaggt 940
Db 901 TTTTAAAGGTTGT 939

RESULT 8
AX282355 956 bp DNA linear PAT 02-NOV-2001
LOCUS AX282355
DEFINITION Sequence 5 from Patent WO0166746.
ACCESSION AX282355
VERSION AX282355.1 GI:16609544
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (sttee)
AUTHORS Padigaru,M., Burgess,C.E., Majumder,K., Mishra,V.S., Li,L.,

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Qy 2 atgaattggtaaatgacagatcatatcaagaaagtattatctgtcgtgtgtgtgtgtgtgt 61
Db 7 ATGAATGGTAATGACAGCATATACAGAGTTATCTGTGAGGTTCTCAGATCGA 66
Qy 62 ccttgctgaggttccactcctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 121
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Qy 122 ggcacatcgacatattatctagtgtaacagcctgagacacacacacacacacacacac 181
Db 127 GGCATATCGACATATTATGATGTGACGCTGACACCAACTTCAATCCCATGTAT 186
Qy 182 tttttcttaacaaactatcaactcctcgatcttcttaccacacacacacacacacacaa 241
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Qy 242 atgtagtaaatatgatgacagatcagaaagaaatcaagttatctgtgtgtgtgtgtgtgt 301
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Qy 302 ctttcataattctgcgcttgggggctactgataatctctcctgcgcgtatgtctctt 361
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Qy 422 tgcctcaagttgagctgacatcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 481
Db 427 TGCTTCAGTTGGAGCTGACATCTGTGGTTACTGTTTAACTGATGATGATGTGTGTCT 486
Qy 482 accctgactctcagctgcgacactctgtgacccctatgtatagatcaactctctgtgaa 541
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Qy 542 gtccctgactgctcaagttatcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 601
Db 547 GTCCCTGACACTGCTCAAGTTATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 606
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Qy 722 tgtgtgtccatcaataattgt 781
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Qy 842 atgtcaccaatgctgaatccctctatatatacacttaggaacaggaaggtaaagaaagc 901

Query Match 99.4%; Score 937.2; DB 6; Length 956;
Best Local Similarly 99.7%; Pred. No. 1,1e-255;
Matches 939; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
FEATURES
source
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BASE COUNT 227 a 228 c 190 g 311 t
ORIGIN

Db	902	tttaaaggcttggttcgaagcgctcttctaatacgaataa	943
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RESULT 9			
HSA302593			
LOCUS			
DEFINITION	HSA302593	1074 bp	DNA
ACCESSION	AJ302593		linear
VERSION	AJ302593.1	GI:12054410	PRI 06-JAN-2001
KEYWORDS	6M1-10*02 gene, olfactory receptor.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1074)		
TITLE	Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck,S.		
JOURNAL	Polymorphic olfactory receptor genes and HLA loci constitute extended haplotypes (in) Kasahara,M. (Ed.); MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION, STRUCTURE, AND FUNCTION: 110-130; Springer-Verlag, Tokyo, Japan (2000)		
REFERENCE	2 (bases 1 to 1074)		
AUTHORS	Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Volz,A., Younger,R.M. and Beck,S.		
JOURNAL	Polymorphisms in olfactory receptor genes: a cautionary note		
REFERENCE	3 (bases 1 to 1074)		
AUTHORS	Younger,R.M., Amadou,C., Bethel,G., Ehlers,A., Fischer,Lindahl,K., Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Trowsdale,J., Volz,A., Ziegler,A. and Beck,S.		
JOURNAL	Characterisation of clustered MHC-linked Olfactory Receptor Genes in Human and Mouse		
TITLE	Unpublished		
JOURNAL	4 (bases 1 to 1074)		
REFERENCE	Ehlers,A., Beck,S., Forbes,S.A., Trowsdale,J., Volz,A., Younger,R. and Ziegler,A.		
AUTHORS	MHC-linked olfactory receptor loci exhibit polymorphism and contribute to extended HLA/OR-haplotypes		
JOURNAL	Unpublished		
TITLE	5 (bases 1 to 1074)		
JOURNAL	Ehlers,A.		
REFERENCE	Direct Submission		
AUTHORS	Submitted (06-NOV-2000) Ehlers A., Institut fuer Immunogenetik, Universitaetsklinikum Charite, Spandauer Damm 130, 14050 Berlin, GERMANY		
FEATURES			
source	Location/Qualifiers		
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gene			
CDS			

BASE COUNT	277 a	248 c	203 g	346 t	ORIGIN
Query Match	77.2%	Score 727.8;	DB 9;	Length 1074;	
Best Local Similarity	86.4%	Pred. No. 4,1e-196;			
Matches	815;	Conservative	0;	Mismatches 127;	Indels 1;
					Gaps 1
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Db	1	ATGAATTTGGGTAAATAAAGAGTGTCCACACGGAGGTTCATCTGTATATTTCACAGTCA	60		
OY	62	ccttgtagtgaaattccactcctcttggtggtctcttbaatcttttaacacgtgtgaccacttt	121		
Db	61	CCATGGCTAGAGATTCCACCCTTTTGTGANTGTTTCGTCTTTTCTATATCTTGGACAATCTTT	120		
OY	122	ggcaactctgaccatattatctagtgtaacgctctggacacccaactcatataccccatgtat	181		
Db	121	GGCAATCTGACATAATATTCTGTGTGCATGAGGATTTCAAACTCCACACCCCTATGTAC	180		
OY	182	ttttttctaccaatctatacactccctgagctctttgttaacacacatgtcaccacaa	241		
Db	181	TTTTTTCTTAGAATCTCTCACTCCGTGACCTTGGATTCGTATACCAAGTACAGTTCACAA	240		
OY	242	atgcataaattatgatgcagcatcaagaaagaatcaatcagttatcgtgtgtgtgaccag	301		
Db	241	ATGCTGTGAACATATATGCAACACAGGAAGTATCATGTATATGTGTGCTGTGTGCCAG	300		
OY	302	ctttcataatctctgagccttgagggtactgaatatctctccctggcgatcgtccctt	361		
Db	301	CTTTTCATTTTCTCTGCGCTTGGGTTCCACAGATGCTTCTCTCCGTACGTATGTCCTT	360		
OY	362	gattggtttgtagcatattgttcgacctcccaattactaagttatcaatgacacgaagac	421		
Db	361	GATAGTGTGTAGCTATTTGTGGCGCTTCCTCAATACTCAATATATCATGACACGAGGCTC	420		
OY	422	tgacctcagttgagcagctgcatccctggttggttactggttttaagtaactcagtggtgtct	481		
Db	421	TGCTTCCAACTTGGGAGCTCATTCCTGTGATTAGGCGTTTATAGCAATTCAGTATACAGTCC	480		
OY	482	aacctgacctcaagctgcacctctgtgagccctatgtagttagatcaactctctctgtga	541		
Db	481	ACCTGGACACTTAAGATGCGCACTGTGTGGTGCACAAAGAAAGTGAATCATTCTTGTGAA	540		
OY	542	gtccctgcactgctcgaagtatctctgtgtgagacaacagcaaatgagctgaactac	601		
Db	541	GTCCCTGCTGTGTGTAAGTTGTGTCGATGTAACAAACAGCAAAATGAGCTGAACTATTC	600		
OY	602	cttgtagtgagatctcttcatactataacccctgagacatcatcttatcatatgctttt	661		
Db	601	TTTCATAGTGTCTATTTCCCTTTAAATACCGGTGACACTCATCTTATTCGTATGCTTTT	660		
OY	662	attgtcgcgagcatattggagatacagctctgctggaagctgcagacaagaacatltggaca	721		
Db	661	ATTGTCCAAAGCACTGTTTGAGAAATCCAGTGTCTGGAAGTGTGCAGAAAGCATTTGGACA	720		
OY	722	tgtgtgtccatcataatgtgtgtgtctcttlttlaagtaacgctgtcctgtgtactgt	781		
Db	721	TGTGTGCTCCCACTAATATTGTGTGTGTCATTTTATGTGTAACAGCTATCTCAGTATCTGT	780		
OY	782	caaccacctctggccccagctccaaagaccaaagaagaatgtttctctctcttatgtaatc	841		
Db	781	CAACCACTTTCACCCAGCTCCAAAGACCGGGGAAATAGTGTCTCTCTGTGTGAATTC	840		
OY	842	attgcacccatctgtaatcccttatataataccttaaggaaagaaggttaaaggaagtc	901		
Db	841	ATTGCAACCATGCTGAATCCCTTATATATPACACTTAGGAACAACAAGGTAAAGGAAGCC	900		
OY	902	tttaaaaggtctggtgc-aagagcttcttaatcaagaataa	943		
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RESULT 10
AX241494 1071 bp DNA Linear PAT 26-SEP-2001
LOCUS Sequence 242 from Patent W00127158.
DEFINITION AX241494
ACCESSION AX241494
VERSION AX241494.1 GI:15798369
KEYWORDS
SOURCE
ORGANISM synthetic construct.
REFERENCE synthetic construct.
AUTHORS artificial sequence.
1 (bases 1 to 1071)
Bellenson,D., Smith,D., Lancet,D., Glusman,G., Fuchs,T. and
Yanal,I.
TITLE Olfactory receptor sequences
JOURNAL Patent: WO 0127158-A 242 19-APR-2001;
Discents (US) : YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
FEATURES
source
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="(H3891 nucleotide)"
BASE COUNT 277 a 248 c 201 g 345 t
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Query Match 77.0%; Score 726.2; DB 6; Length 1071;
Best Local Similarity 86.3%; Pred. No. 1.2e-195;
Matches 814; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

QY 2 atgaatgggttaaatgacgacatcatcagaaggttattctgctgggttctcagaatcga 61
DB 1 ATGAATGGGTAAATAAGAGTGCACAGAGTTCATCTGTAGATTCTCGAGATCAA 60
QY 62 cctggagctgagttcaccctctgctgctctctgattctcttaccatgagccatctt 121
DB 61 CCATGGCTAAGATTCACCCCTTTGTGATGTCTGTCTGTTCCATATCTGACATCTTT 120
QY 122 ggaacatgcacattatctagtagtcagcctgagacacaaacttaacccccatgat 181
DB 121 GGCATATGTGCAATATATCTTGTGTGCATGTGATGATTTCAAACTCCACACCCCTATGTAC 180
QY 182 tttttcttccatctatctactcctgtagctcttgtagtccacatgtaagtcacca 241
DB 181 TTTTCTTCTTGCAATCTCTACTCTGGACCTTGTGATCAACAATGATGATTCACAA 240
QY 242 atgctaaatattatgcagatcagaagaagtaaatcagttatcgtgctgtgagccag 301
DB 241 ATGCTGTAAACATATTCACACACAGGAAGTAAATCATGATGTGCTGTGCGCCAG 300
QY 302 ctttcaattctcggccttgggggactgaatctctcctggcgcgtcatgctctt 361
DB 301 CTTTCTATTTCTTCCTGGCCTTGGGTTCCACAGAAATGCTTCTCCGCGCCGATGCTTT 360
QY 362 gattggttttagctatttctggcctctcattactacacattatcagaccagaagctc 421
DB 361 GATAGGTTTATGCTATTTCTGCGCCTCTCATATTACATATACAGCACCGAGGCTC 420
QY 422 tggctcagtttgcagctgacatcctgggttactggttttagtaactaagtggttct 481
DB 421 TGGCTTCAGTTGGAGCTGATCOTGATTAAGTGGCTTTGACAAATTCAGATTACATCC 480
QY 482 accctgaactcgaagctgcacactctgtgaccctcatatgtagatgaactcttctgtga 541
DB 481 ACCCTGACACTTAAAGAGCCACTGTGTGTGCACAAAGAAATGATGATCACTTCTCTGTGA 540
QY 542 gtccctgcaactgctcaagttatcttgggtgagagaaacaaatgagggctggaacttc 601
DB 541 GTCCCTGCTCTGCTCAAGTTGTCTGTGTGACACACAAATGAGGCTGAGACTATTC 600
QY 602 ctgtcagtagactcttcaatcctaataacccccagacactacactatataatgctctt 661
DB 601 TTTCATGAGTGTGCTATTCCTTAAATACCGGTGACACTCATCTTAAATGATGCTTT 660

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QY 662 atgtccgagcagttatgagatcacagtcgtcgtgaaggttcgacaaaagcattgggaca 721
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QY 842 atgacaccaatgctgaatcccttatataatacactttagaacaagaaggtgaaggaagc 901
DB 841 ATTGACACCAATGCGATTCCTTATATATCACTTGAACAAAGAGTGAAGGAGGCC 900
QY 902 tttaaaaggttggtgc-aagagctctcttaatcaagaataa 943
DB 901 TTTAAAAGTGTGTTGCCAAGAGTCTTATATCAAGAAATAA 943

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RESULT 11
AX242075 1071 bp DNA Linear PAT 26-SEP-2001
LOCUS Sequence 823 from Patent W00127158.
DEFINITION AX242075
ACCESSION AX242075
VERSION AX242075.1 GI:15798950
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE artificial sequence.
1 (bases 1 to 1071)
Bellenson,D., Smith,D., Lancet,D., Glusman,G., Fuchs,T. and
Yanal,I.
TITLE Olfactory receptor sequences
JOURNAL Patent: WO 0127158-A 823 19-APR-2001;
Discents (US) : YEDA RESEARCH AND DEVELOPMENT COMPANY, LTD. (IL)
FEATURES
source
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/organism="synthetic construct"
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/note="(H38973 nucleotide)"
BASE COUNT 277 a 248 c 201 g 345 t
ORIGIN

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Query Match 77.0%; Score 726.2; DB 6; Length 1071;
Best Local Similarity 86.3%; Pred. No. 1.2e-195;
Matches 814; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

QY 2 atgaatgggttaaatgacgacatcatcagaaggttattctgctgggttctcagaatcga 61
DB 1 ATGAATGGGTAAATAAGAGTGCACAGAGTTCATCTGTAGATTCTCGAGATCAA 60
QY 62 ccttgctgagtttccaccccttgggtctctctttagattcttaacactgagacatctt 121
DB 61 CCATGGCTAAGATTCACCCCTTTGTGATGTCTGTCTGTTCCATATCTGACATCTTT 120
QY 122 ggaacatgcacattatctagtagtcagcctgagacacaaacttaacccccatgat 181
DB 121 GGCATATGTGCAATATATCTTGTGTGCATGTGATGATTTCAAACTCCACACCCCTATGTAC 180
QY 182 ttttttcaacaatctatcactcctgtagctctgtgtacacacatgtagtaccacaa 241
DB 181 TTTTCTTCTTGCAATCTCTCACTCTGACCTTGTGATATCCACAGATACAGTTCCACA 240
QY 242 atgctaaatattatgacagcatcagaagaagtaaatcagttatcgtggtctgtgagccag 301
DB 241 ATGCTGTAAACATATTCACACAGGAAGTAAATCATGATGTGCTGTGCGCCAG 300
QY 302 ctttcaattctcggccttgggggactgaatctctcctggcgcgtcatgctctt 361
DB 301 CTTTCTATTTCTTCCTGGCCTTGGGTTCCACAGAAATGCTTCTCCGCGCCGATGCTTT 360

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Db 301 CTTTTCATTTTCTGCGCTTGGGTTCCACAGATGTCCTCTCTGCGCGCATGTCCTTT 360
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Db 361 GATAGGTTTGTAAGCTATTTGTCGGCTCTTCATTAATCAATATGACACAGAGAGCTC 420
QY 422 tgcctcagttgagctcactcactggttactggttttagtaaccagtggtgtctc 481
Db 421 TGCTTCACATTTGACACTGACCTGATCCGTGATTAAGGCTTTAGCAATTCAGATTACAGCTC 480
QY 482 accctgactctcagctgacgtcactctgtgacccctatgatatagatcacttctctgaa 541
Db 481 ACCTGACACTTAAGATGACACTGTCGTGTCACAAAGAGTGCATCTTCTCTGTGAA 540
QY 542 gtccctgacgtcctcaagtatctgtgtgtgagacacagcaaatgaggtcgaactatc 601
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Db 841 ATGACACCATGCTGATCCCTTATATATACACTAGAGACAAAGAGTAAGGAAGCC 900
QY 902 tttaaaagttgtgtgc-aagagctcttctaatacaagaataa 943
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RESULT 12
HSA302584 1074 bp DNA linear PRI 06-JAN-2001
LOCUS HSA302584
DEFINITION Homo sapiens 6M1-10*01 gene for olfactory receptor, cell line BM28.7.
ACCESSION AJ302584
VERSION AJ302584.1 GI:12054392
KEYWORDS 6M1-10*01 gene; olfactory receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Volz,A.,
Trowsdale,J., Younger,R., Younger,R.M., and Beck,S.
TITLE Polymorphic olfactory receptor genes and HLA loci constitute extended haplotypes
JOURNAL (in) Kasahara,M. (Ed.):
MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION, STRUCTURE, AND
FUNCTION: 110-130;
REFERENCE 2 (bases 1 to 1074)
AUTHORS Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Volz,A.,
Younger,R.M., and Beck,S.
TITLE Polymorphisms in olfactory receptor genes: a cautionary note
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1074)
AUTHORS Younger,R.M., Amadou,C., Bethel,G., Ehlers,A., Fischer,Lindahl,K.,
Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Trowsdale,J.,
Volz,A., Ziegler,A. and Beck,S.

TITLE Characterisation of clustered MHC-linked Olfactory Receptor Genes
JOURNAL in Human and Mouse
REFERENCE Unpublished
AUTHORS 4 (bases 1 to 1074)
Ehlers,A., Beck,S., Forbes,S.A., Trowsdale,J., Volz,A., Younger,R.,
Ziegler,A.
TITLE MHC-linked olfactory receptor loci exhibit polymorphism and
contribute to extended HLA/OR-haplotypes
JOURNAL Unpublished
REFERENCE 5 (bases 1 to 1074)
AUTHORS Ehlers,A.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2000) Ehlers A., Institut fuer Immunogenetik,
Universitaetsklinikum Charite, Spandauer Damm 130, 14050 Berlin,
GERMANY

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AFIVQAVLRIOGAEQKRAFCGSLIVSLSFGTAISMVLOPPSPSKDKGNVSL
FCGIIAPMLNPLIYLRNKEVKAERKRLVAKSLINDEIRNMOMISFADTVLYTLNF
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BASE COUNT 278 a 248 c 202 g 346 t
ORIGIN

Query Match 77.0%; Score 726.2; DB 9; Length 1074;
Best local Similarity 86.3%; Pred. No. 1.2e-195;
Matches 814; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

QY 2 atgaattgggtaaatgacagcatalcacaagaggttattctgtcgtgggttcagaatcga 61
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QY 122 ggcacatgcacattattctagtgtaacgcgtggaaccaaaactcatatcacccatgta 181
Db 121 GGCATCTGCATTAATTTCTTGTGTCAATGTGATTTGAAATCCACAGCCCTATGTAC 180
QY 182 tttttcttaccatcatcactcctggaactctgtgtataccacatgtaacagtcacaa 241
Db 181 TTTTCTTGAACATCTCCTCCTGAGACCTTGTGTAATCCACAGATGACAGTTCCACAA 240
QY 242 atgctagtaaatltagcagcagcaagaagtaatacagttatcgtgtgctgtgaagccag 301
Db 241 ATGCTGTAACATATGCAACACAGAAAGTAATCAGTTATGAGTGTGTGGGCCAG 300
QY 302 cttaataattctggccttggggcgtgactgaatactcttctcgtggcgtgcatgctctt 361
Db 301 CTTTTCATTTTCTGCGCTTGGGTTCCACAGATGTCCTCTCTGCGCGCATGTCCTTT 360
QY 362 gattggtttgtagctatttgcggcctccatctactcagttatcatgacacagagactc 421
Db 361 GATAGGTTTGTAAGCTATTTGTCGGCTCTTCATTAATCAATATGACACAGAGAGCTC 420
QY 422 tgcctcagttgagctcactcactggttactggttttagtaaccagtggtgtctc 481

Db 421 TGCTTCAGTTGGCAGCTGCATCTCGATTAGTGGCTTTAGCAATTCAGATTACACATCC 480
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OY 602 ctgtcagtgagctcttcacatcctaacccctgacacatccttatacatatgcttc 661
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OY 662 attgtcgaagcagatgagatgagatacagctcgtcgaagcgtcgaacaaagcattggaga 721
Db 661 ATTGTCCAAACAGTGTGAATTCACATCTGCTGCAAGGTACACGAAGGCAATTTGGGACA 720
OY 722 tctgtgtcccatcctaattgtgtgtcctcttcttatagtacagcgtcgtgtgacctg 781
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Db 841 ATTGACACCCATGCTGAATCCCTTATATATACACTTATGGAACAAAGAGTAAAGGAGCC 900
OY 902 tttaaaagtggtgtgc-aagagctcttctaacaagaataa 943
Db 901 TTTAAAGGTTGGTGTGCAAGAGTCTTCTTAATCAAGAAATTA 943

RESULT 13
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LOCUS Homo sapiens 6M1-10*01 gene for olfactory receptor, cell line
DEFINITION BM19.7.
ACCESSION AJ302585
VERSION AJ302585.1 GI:12054394
KEYWORDS 6M1-10*01 gene; olfactory receptor.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1074)
AUTHORS Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J.,
TITLE uchanska-Ziegler, B., Volz, A., Younger, R. and Beck, S.
Polymorphic olfactory receptor genes and HLA loci constitute
extended haplotypes
(in) Kasahara, M. (Ed.):
MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION, STRUCTURE, AND
FUNCTION: 110-130.
Springer-Verlag, Tokyo, Japan (2000)
REFERENCE 2 (bases 1 to 1074)
AUTHORS Ziegler, A., Ehlers, A., Forbes, S.A., Trowsdale, J., Volz, A.,
TITLE Younger, R.M. and Beck, S.
Polymorphisms in olfactory receptor genes: a cautionary note
Unpublished
3 (bases 1 to 1074)
JOURNAL Younger, R.M., Amadou, C., Bethel, G., Ehlers, A., Fischer, Lindahl, K.,
REFERENCE Forbes, S.A., Horton, R., Milne, S., Mungall, A.J., Trowsdale, J.,
AUTHORS Volz, A., Ziegler, A. and Beck, S.
Characterisation of clustered MHC-linked Olfactory Receptor Genes
in Human and Mouse
Unpublished
4 (bases 1 to 1074)
JOURNAL Ehlers, A., Beck, S., Forbes, S.A., Trowsdale, J., Volz, A., Younger, R.
REFERENCE and Ziegler, A.
AUTHORS MHC-linked olfactory receptor loci exhibit polymorphism and

contribute to extended HLA/OR-haplotypes
Unpublished
5 (bases 1 to 1074)
REFERENCE Ehlers, A.
AUTHORS Direct Submission
TITLE Submitted (06-NOV-2000) Ehlers, A., Institut fuer Immunogenetik,
JOURNAL Universitaetsklinikum Charite, Spandauer Damm 130, 14050 Berlin,
GERMANY
FEATURES
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FCGIAPMLNPLITLRLNKEKEAFKRLVAKSLNDELIRNMOMISFAKDTVLYTLNF
SASCFEVIETINCYMLPORKRP"

BASE COUNT 278 a 248 c 202 g 346 t
ORIGIN

Query Match 77.0%; Score 726.2; DB 9; Length 1074;
Best local Similarity 86.3%; Pred. No. 1.2e-195;
Matches 814; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

OY 2 atgaattgggtaaatgacagcatcacaagagattactcgtcgtggttctcaatcga 61
Db 1 ATGAATGGCTAAATTAAGAGTGTCCACAGAGACTTCATCTGTAGCTTTCTCAGATCA 60
OY 62 ccttgctgagagttcgaacccctcgtgtgtccttcttacttcaactgagacactctt 121
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OY	722	tgttgctcccatcaatctgtgtgtctctcttttaatagtacacgcctctgtacctg	781
Db	721	TGTGCTGCCAATCTTAATGTGTGTGCACATTTTATTNGGTACAGCATATCTCATGTACTCG	780
OY	782	caaccacacttgcgccagctccaagaaccaagaagaatggttctctcttcataygatc	841
Db	781	CAACCACCTTCACCCAGCTCCAAAACCGGGAAGAATGTTCCTCTCTGTGGAAAC	840
OY	842	attgcaccatctgaatcccccttatatatatacacttagaacagaaggtaaagaagc	901
Db	841	ATTGCACCACTTCCTGAATCCCCTTTATATATACACTTAGAACAAAGAGTAAAGAACCC	900
OY	902	tttaaaagttgtgtgc-aagaagctctcttaatacaagaataa	943
Db	901	TTTAAAGTGTTGTCAAAGAGCTCTTCTATATCAAGAAATGA	943
RESULT 15			
LOCUS	HSA302587	1074 bp	DNA
DEFINITION	Homo sapiens 6M1-10*01 gene for olfactory receptor, cell line H2LC.		linear PRI 06-JAN-2001
ACCESSION	AJ302587		
VERSION	AJ302587.1	GI:12054398	
KEYWORDS	6M1-10*01 gene; olfactory receptor.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 1074)		
TITLE	Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Uchanska-Ziegler,B., Volz,A., Younger,R. and Beck,S. Polymorphic olfactory receptor genes and HLA loci constitute extended haplotypes		
JOURNAL	(in) Kasahara,M.(Ed.): MAJOR HISTOCOMPATIBILITY COMPLEX-EVOLUTION, STRUCTURE, AND FUNCTION: 110-130;		
REFERENCE	Springer-Verlag, Tokyo, Japan (2000)		
AUTHORS	2 (bases 1 to 1074)		
TITLE	Ziegler,A., Ehlers,A., Forbes,S.A., Trowsdale,J., Volz,A., Younger,R.M. and Beck,S. Polymorphisms in olfactory receptor genes: a cautionary note		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1074)		
AUTHORS	Younger,R.M., Amadou,C., Bethel,G., Ehlers,A., Fischer,Lindahl,K., Forbes,S.A., Horton,R., Milne,S., Mungall,A.J., Trowsdale,J., Volz,A., Ziegler,A. and Beck,S. Characterisation of clustered MHC-linked Olfactory Receptor Genes in Human and Mouse		
TITLE	Unpublished		
JOURNAL	4 (bases 1 to 1074)		
REFERENCE	Ehlers,A., Beck,S., Forbes,S.A., Trowsdale,J., Volz,A., Younger,R. and Ziegler,A. MHC-linked olfactory receptor loci exhibit polymorphism and contribute to extended HLA/OR-haplotypes		
AUTHORS	Unpublished		
TITLE	5 (bases 1 to 1074)		
JOURNAL	Ehlers,A. Direct Submission Submitted (06-NOV-2000) Ehlers A., Institut fuer Immunogenetik, Universitaetsklinikum Charite, Spandauer Damm 130, 14050 Berlin, GERMANY		
FEATURES			
SOURCE	Location/Qualifiers		
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Query Match	Best Local Similarity	Matches	814; Conservative	77.0%; Score 726.2; DB 9; Length 1074;	86.3%; Pred. No. 1.2e-195;	0; Mismatches 128; Indels 1; Gaps 1;
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Qy	122	ggcaatctgacattatcttagtgcacgacctggagacaccaactcatataccccaatgat	181	TWTKMLPGKGEVDHFECEVPALDKLSCTVDPTNEMLEFISVFLIPTVLLIS	AFIYQAVLRISAGSGORAKAFTGCSHLIVSLFPGTASIMSLQPSSESKDRGMVSI	
Db	121	GGCAATCTGACAAATATTTCTTGTGTCACATGTGGATTTCAAACTCCACACCCCTATGTC	180	FCGIAPFLNPLIYTLNRKEVEAKFRVLKASLLNQEIRNMQMISFANDPVLTLTNE	SASCPFIPIETENCNLPORKEP"	
Qy	182	tttttctaccatctatcaactcctctgtaactcttcttctaacacacatgtaacgtccaca	241			
Db	181	TTTTTCTTAGCAATCTCTCACTCCGTGGACCTTTGCTATACCAAGTACATGTTCCACAA	240			
Qy	242	atgcagtaaatattatgcagacatcaaggaaagtaacagatcatcggtctgtgttagccag	301			
Db	241	ATGCTGGTAAACATATATGCAACACAGGAAAGTAATCAGTTATGATGTCGTGTGGCCAG	300			
Qy	302	ctttcatattctctggccttggggacctgaatgaaatctctctctggccgtacatgctctt	361			
Db	301	CTTTTCATTTTCTGTGGCCTTGCGCTTCACAGAAATGCTTCTCTGCGCTCATGTGCTTT	360			
Qy	362	gattgtctgtatctatttctgcgacctcccaactcaactcaatcatatgcacaagaagac	421			
Db	361	GATAGTGTGTGATGATTTGTGCGGCTGTCCATTAATCAATATCATGACACAGAGGCTC	420			
Qy	422	tgcctcagattggcagctgcacatcctggtgttactggtctttagtaacctcagtggtgtct	481			
Db	421	TGCTTCCAGTGGGACGCTGCATCTCGAATTAATGAGCTTTAGCAAAATTCAGTATTACAGTCC	480			
Qy	482	accctgactctccagctgcacatcgtgtaacccctatgtagatagatcaacttctcgtgtaa	541			
Db	481	ACCTGAGACACTTAATATGACCTGTGTGTCACAAAGAGTGAATCATTCTTCTGTGTA	540			
Qy	542	gtccctgcacatcgtcaaatatctctgtgtgtgagacaagaacaaagagctgaactatctc	601			
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Db	601	TTCATCAGTGTGCTATTCCTCTTAATATACCGGACACATCATCTTAATATGATGATCTTTT	660			
Qy	662	attgtccgaagcagtatctgaagataagtcctgctgtaaggtcgacaacaaaagactttggaca	721			
Db	661	ATTGTCCAAAGCAGTGTGGAATCCAGTCTGCTGAAGGTCAACGAAAGCAATTGGGACA	720			
Qy	722	tgtgttcccatcaatattgtgtgtctcttttttagtaagcgtctctgtgtactgt	781			
Db	721	TGTGTCTCCATCTAATATGTGTGTGCTCTTTTATATGATGACGCTATATCTCATATGACTGTG	780			

OY 782 caaccaccttcgcccagctcccaaggaccaaggaagatggttctctctctatggaatc 841
Db 781 CAACCACTTCACCCAGCTCCAAAGACCGGGAAAGATGGTTCTCTCTGTGAATC 840
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Db 841 ATTGCACCCATGCTGAATCCCTTATATATACCTTAGGAACAAGAGTAAAGGAAGCC 900
OY 902 tttaaaagtggttgc-aagagctctctaatacagaataaa 943
Db 901 TTTAAAGGTTGTTGCAAGAGTCTTATATCAGCAATAAA 943

Search completed: August 25, 2002, 18:57:02
Job time: 14460 sec

CDS

sig_peptide

mat_peptide

/product= "Mature GPCR NOV1b protein"

WO20016746-A2.

13-SEP-2001.

05-MAR-2001; 2001MO-US07116.

03-MAR-2000; 2000US-0186606.
06-MAR-2000; 2000US-0187247.
06-MAR-2000; 2000US-0187248.
06-MAR-2000; 2000US-0187249
06-MAR-2000; 2000US-0187250.
06-MAR-2000; 2000US-0187253.
06-MAR-2000; 2000US-0187295.
06-MAR-2000; 2000US-0187296.
07-MAR-2000; 2000US-0187563.
21-JUL-2000; 2000US-0219854.
24-JUL-2000; 2000US-0220253.
31-JUL-2000; 2000US-0221942.
21-DEC-2000; 2000US-0257600.
08-Jan-2001; 2001US-0260285.

(CURA-) CURAGEN CORP.

Patigaru M., Burgess CE, Majumder K, Mishra VS, Li L;
Baumgartner JC, Spytek KA, Tchernev VT;

WP1; 2001-565586/63.
P-PSTDB; AAE09961.

Noval polypeptides designated as NOVX polypeptides, useful in detection, prevention and treatment of e.g. Parkinson's disease and Cancer -

Claim 8; Page 10; 174pp; English.

The invention relates to novel G-protein coupled receptor (GPCR) related peptides and their corresponding nucleotides, referred as NOVX or NOVY, NOVZ, NOVU, NOVW, NOV5, NOV6, NOV7, NOV8, NOV9 and NOV10. NOVX and its Ab are useful for treating or preventing a NOVX-associated disorder, such as disorder related to cell signal processing and metabolic signal pathway modulation, e.g. diabetes. Pharmaceutical composition comprising NOVX sequence is used to treat or prevent disorders or syndromes including metabolic disturbances associated with obesity, anorexia, wasting disorders associated with chronic diseases, infectious diseases (particularly infections caused by HIV-1 or HIV-2), cancer-associated cachexia, cancer, Parkinson's disease, Alzheimer's disease, immune disorders, neurodegenerative diseases and haematopoietic disorders. NOVX sequence is also useful for treating developmental disorders. NOVX histocompatibility complex (MHC) II and III diseases (immune diseases), noninsulin-dependent diabetes mellitus (NIDDM1), bulimia, hypotension, acute heart failure, multiple sclerosis, hypertension, osteoporosis, Crohn's disease, Albrignt Hereditary Osteodysrrophy, angina pectoris, myocardial infarction, asthma, allergies, benign prostatic hypertrophy CC and psychotic and neurological disorders, including anxiety, delirium, schizophrenia, manic depression, dementia, severe mental retardation, dentatorubropallidoluysian atrophy (DRPLA) hypophosphataemic rickets, autosomal dominant (2) acrocallosal syndrome and dyskinesias, such as Huntington's disease or Gilles de la Tourette syndrome and/or other pathologies. NOVX DNA is used in mapping the chromosomal location of NOVX gene and in forensic biology. The present sequence is GPCR NOV1b DNA.

Sequence 943 BP; 221 A; 227 C; 187 G; 308 T; 0 other:

Query Match	100.0%	Score 943:	DB 227:	Length 943:	
Best Local Similarity	100.0%	Pred. NO. 5.7e-277:			
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					Gaps
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DB	1	tatgatattggtggaataatgacagcatcatacaagaagatttaattcgtctggtgtttctcagatcg	60		
OY	61	accttggtctgtaggtttccaaactcctctgtgtgtcttcttgattcttcaactgtgacaactt	120		
DB	61	accttggtctgtaggtttccaaactcctctgtgtgtcttcttgattcttcaactgtgacaactt	120		
OY	121	tggcgaatctgaccatattatcttagtgtcaacgcttggaacccaactcaaaccccatgtga	180		
DB	121	tggcgaatctgaccatattatcttagtgtcaacgcttggaacccaactcaaaccccatgtga	180		
OY	181	ttttcttcttaaccaatcatactcaactcctgtgattctgtttaaccaacatgtatagaatccaca	240		
DB	181	ttttcttcttaaccaatcatactcaactcctgtgattctgtttaaccaacatgtatagaatccaca	240		
OY	241	aatgctaagtaaatattatgacagcatcaagaagaatcaagttacgtatcgtgtgtgtgccca	300		
DB	241	aatgctaagtaaatattatgacagcatcaagaagaatcaagttacgtatcgtgtgtgtgccca	300		
OY	301	gctttccatattctggcgcttggggcgccactgaatatattctccggcgccgcatatccct	360		
DB	301	gctttccatattctggcgcttggggcgccactgaatatattctccggcgccgcatatccct	360		
OY	361	tgatgtgtttgttagactaattgtgcgacctccatctactcaatgaattacatcatgacacagaagact	420		
DB	361	tgatgtgtttgttagactaattgtgcgacctccatctactcaatgaattacatcatgacacagaagact	420		
OY	421	ctgctctcaagtctggcagctgtcatctctgtgttactctgtgttttagtaactcaagtgtgttctc	480		
DB	421	ctgctctcaagtctggcagctgtcatctctgtgttactctgtgttttagtaactcaagtgtgttctc	480		
OY	481	taccttgactctccagcgcgcgcacactctgtgaaaccccatgtgataagataactctctgtgga	540		
DB	481	taccttgactctccagcgcgcgcacactctgtgaaaccccatgtgataagataactctctgtgga	540		
OY	541	agtcctctgactgtctcaagttaactctgtgtgttgagacaacacagcaaaatgtgagctgtaactat	600		
DB	541	agtcctctgactgtctcaagttaactctgtgtgttgagacaacacagcaaaatgtgagctgtaactat	600		
OY	601	cccttgtaagtggagcctctccatcataataacccctggacactccatcccttatataataatgcttt	660		
DB	601	cccttgtaagtggagcctctccatcataataacccctggacacactccatcccttatataataatgcttt	660		
OY	661	tatttccgagagagatttgaagatacaactctgtctgtaaagtcgacacaaaagacatttgggac	720		
DB	661	tatttccgagagagatttgaagatacaactctgtctgtaaagtcgacacaaaagacatttgggac	720		
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DB	721	atgtgtgttcccatctaattgtgtgtctctcttattatagtaaacgcgctctctgtgtact	780		
OY	781	gcaaccacctctggccagactccaagaagacaaagaaagatgttcttccctcttaagaaat	840		
DB	781	gcaaccacctctggccagactccaagaagacaaagaaagatgttcttccctcttaagaaat	840		
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RESULT	2				
AAAD17015					
ID	AAAD17015	standard; DNA; 993 BP.			

XX	AC		AD17015;	
XX	AD		29-NOV-2001	(first entry)
XX	DE		G-protein coupled-receptor (GPCR) NOVA DNA.	
KW	KM		G-protein coupled-receptor; GPCR; NOVA-associated disorder; obesity;	
KW	KM		anorexia; wasting disorder; infection; cachexia; Parkinson's disease;	
KW	KM		Alzheimer's disease; immune disorder; neurodegenerative disease; cancer	
KW	KM		anorectic; haemotopoietic disorder; major histocompatibility complex;	
KW	KM		MHCII; noninsulin-dependent diabetes mellitus; NIDDM; bulimia; asthma;	
KW	KM		acute heart failure; hypotension; multiple sclerosis; hypertension;	
KW	KM		osteoporosis; Crohn's disease; mental retardation; dementia; allergy;	
KW	KM		angina pectoris; myocardial infarction; benign prostatic hypertrophy;	
KW	KM		psychotic disorder; neurological disorder; anxiety; schizophrenia;	
KW	KM		manic depression; delirium; Albright Hereditary Osteodystrophy; rickets	
KW	KM		dentalorodopallidolysian atrophy; DRPIA; haemostatic; anticonvulsant;	
KW	KM		autosomal dominant (2) acrocallosal syndrome; dyskinesia; neuroleptic;	
KW	KM		Huntington's disease; Gilles de la Tourette syndrome; neuroprotective;	
KW	KM		neotropic; antibacterial; protozoacide; fungicide; cytostatic; NOVA;	
KW	KM		vulnerary; cardiant; osteopathic; antiingnal; anticulcer; virucide;	
KX	XO		human immunodeficiency virus; HIV; antidepressant; tranquilliser; ds.	
XX	OS		unidentified.	
FT	FH		Key	Location/Qualifiers
FT	FT		5'UTR	1..14
FT	FT		CDS	/tag= a 15..96
FT	FT			/tag= b
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FT	FT			15..128
FT	FT		mat_peptide	/tag= c 129..953
FT	FT			/tag= d
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XX	PN			/tag= e
XX	PD		MO20016746-A2.	
XX	XX		13-SEP-2001.	
PE	PF		05-MAR-2001; 2001WO-US07116.	
PR	PR		03-MAR-2000; 2000US-0186606.	
PR	PR		06-MAR-2000; 2000US-0187247.	
PR	PR		06-MAR-2000; 2000US-0187248.	
PR	PR		06-MAR-2000; 2000US-0187249.	
PR	PR		06-MAR-2000; 2000US-0187250.	
PR	PR		06-MAR-2000; 2000US-0187253.	
PR	PR		06-MAR-2000; 2000US-0187295.	
PR	PR		06-MAR-2000; 2000US-0187296.	
PR	PR		07-MAR-2000; 2000US-0187553.	
PR	PR		21-JUL-2000; 2000US-0219854.	
PR	PR		24-JUL-2000; 2000US-0220263.	
PR	PR		31-JUL-2000; 2000US-0221942.	
PR	PR		21-DEC-2000; 2000US-0257600.	
PR	PR		08-JAN-2001; 2001US-0260285.	
XX	PA		(CURA-) CURAGEN CORP.	
XX	PI		Padigaru M, Burgess CE, Majumder K, Mishra VS, Li L;	
XX	PI		Baumgartner JC, Spytek KA, Tchernev VT;	
DR	DR		WPI; 2001-565586/63.	
XX	XX		P-PsDB; AAE09960.	
PT	PT		Novel polypeptides designated as NOVA polypeptides, useful in	
PT	PT		detection, prevention and treatment of e.g. Parkinson's disease and	
XX	XX		Cancer -	

P5		Claim 8; Page 8; 17app; English.
XX		The invention relates to novel G-protein coupled receptor (GPCR) related
CC		polypeptides and their corresponding nucleotides, referred as NOVX or
CC		NOVY, NOVZ, NOV4, NOV5, NOV6, NOV7, NOV8, NOV9 and NOV10. NOVX and
CC		its Ab are useful for treating or preventing a NOVX-associated disorder,
CC		such as disorder related to cell signal processing and metabolic signal
CC		pathway modulation, e.g. diabetes. Pharmaceutical composition comprising
CC		NOVX sequence is used to treat or prevent disorders or syndromes
CC		Including metabolic disturbances associated with obesity, anorexia
CC		(particularly infections caused by HIV-1 or HIV-2), cancer-associated
CC		cachexia, cancer, Parkinson's disease, Alzheimer's disease, immune
SQ		disorders, neurodegenerative diseases and haematopoietic disorders. NOVX sequence is also useful for treating developmental diseases, major histocompatibility complex (MHC) II and III diseases (immune depression, noninsulin-dependent diabetes mellitus (NIDDM)), bulimia, hypotension, acute heart failure, multiple sclerosis, hypertension, osteoporosis, Croun's disease, Alpbright Hereditary Osteodystrophy, angina pectoris, myocardial infarction, asthma, allergies, benign prostatic hypertrophy and psychotic and neurological disorders, including anxiety, delirium, schizophrenia, manic depression, dementia, severe mental retardation, dentatorubral pallidoluysian atrophy (DRPLA) hypophosphataemic rickets, autosomal dominant (2) acrocallosal syndrome and dyskinesias, such as Huntington's disease or Gilles de la Tourette syndrome and/or other pathologies. NOVX DNA is used in mapping the chromosomal location of NOVX gene and in forensic biology. The present sequence is GPCR NOVLA DNA. Sequence 993 BP; 246 A; 233 C; 194 G; 320 T; 0 other; Query Match 99.7%; Score 940.4; DB 22; Length 993: Best Local Similarity 99.9%; Pred. No. 3,6e+276; Matches 941; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 3

AA508541
ID AA508541 standard; cDNA; 942 BP.

AC AA508541;

DT 26-SEP-2001 (first entry)

XX DNA encoding novel human G-protein coupled receptor (NGPCR).

KW Human: novel G-protein coupled receptor; NGPCR; drug discovery;

KW diagnostic; ss.

XX Homo sapiens.

FT Key Location/Qualifiers

FT CDS 1..942 /tag-a

XX /product- "Novel G-protein coupled receptor (NGPCR)"

PN MO200151634-A1.

PD 19-JUL-2001.

PF 05-JAN-2001; 2001WO-US00589.

PR 12-JAN-2000; 2000US-0175764.

XX (LEXI-) LEXICON GENETICS INC.

XX Walke DW, Miljanowski NL, Turner CA, Friedrich G, Abuin A;

PI Zambrowicz B, Sands AT;

XX WPI; 2001-442145/47.

DR P-PSDB; AA004689.

XX New human G-protein-coupled receptor and polynucleotides encoding the

PT receptor, useful in identifying, selecting or validating new molecular

XX targets for drug discovery and in diagnostic or prognostic assays -

PS Claim 1; Page 61; 65pp; English.

CC The sequence represents the coding sequence of novel human G-protein

CC coupled receptor (NGPCR). The NGPCR nucleic acid and protein are useful

CC in identifying, selecting or validating novel molecular targets for drug

CC discovery, as well as in diagnostic or prognostic assays. These are also
CC useful in microarrays or other assay formats, for screening collections
CC of genetic material from patients who have a particular medical condition
CC or for identifying mutations associated with a particular disease.
XX
SQ Sequence 942 BP; 222 A; 228 C; 187 G; 305 T; 0 other:

Query Match 99.6%; Score 938.8; DB 22; Length 942;

Best local Similarity 99.6%; Pred. No. 1.1e-275;

Matches 940; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 atgaattgggtaaatgacagacatcaacagagttattctgtcgtgggttcacagatcga 60
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Db 361 gattgtgttgtagctattctgtggtcctccatcaatccatcaatcaatgacccagagatc 420
Qy 422 tgcctcagcttgagagctgcatctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 481
Db 421 tgcctcagcttgagagctgcatctcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
Qy 482 accctgacttcagctcagctcagctcagctcagctcagctcagctcagctcagctcag 541
Db 481 accctgacttcagctcagctcagctcagctcagctcagctcagctcagctcagctcag 540
Qy 542 gtccctgactgtccaagtatattctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 601
Db 541 gtccctgactgtccaagtatattctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
Qy 602 ctgttcagtagagctcttcacatcaataccctgtgacatcccttatatacatatgcttc 661
Db 601 ctgttcagtagagctcttcacatcaataccctgtgacatcccttatatacatatgcttc 660
Qy 662 attgtccgagcagatattgagatacagctgtctgaagagtcagacaaaagcattgggaca 721
Db 661 attgtccgagcagatattgagatacagctgtctgaagagtcagacaaaagcattgggaca 720
Qy 722 tgtgtgtcccatcaatattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 781
Db 721 tgtgtgtcccatcaatattgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
Qy 782 caaccaccttcgcccagctccaagaggaagatgtttctctctctatgagatc 841
Db 781 caaccaccttcgcccagctccaagaggaagatgtttctctctctatgagatc 840
Qy 842 attgcaccatgtcgtgaatcccttatataacacttagaacaagagtgtaaggaagc 901
Db 841 attgcaccatgtcgtgaatcccttatataacacttagaacaagagtgtaaggaagc 900
Qy 902 tttaaaaggttggttgcaagagctcttcttaatacaagaataa 943


```
FT      /*tag- e
XX      WO200166746-A2.
PN      13-SEP-2001.
XX      05-MAR-2001; 2001WO-US07116.
XX      03-MAR-2000; 2000US-0186606.
XX      06-MAR-2000; 2000US-0187247.
XX      06-MAR-2000; 2000US-0187248.
XX      06-MAR-2000; 2000US-0187249.
XX      06-MAR-2000; 2000US-0187250.
XX      06-MAR-2000; 2000US-0187253.
XX      06-MAR-2000; 2000US-0187295.
XX      06-MAR-2000; 2000US-0187296.
XX      07-MAR-2000; 2000US-0187563.
XX      21-JUL-2000; 2000US-0219854.
XX      24-JUL-2000; 2000US-0220263.
XX      31-JUL-2000; 2000US-0221942.
XX      21-DEC-2000; 2000US-0257600.
XX      08-JAN-2001; 2001US-0260285.
XX      (CURA-) CURAGEN CORP.
XX      Padigarnu M, Burgess CE, Majumder K, Mishra VS, Li L;
PI      Baumgartner JC, Spytek KA, Tchernev VT;
XX      WPI: 2001-565586/63.
XX      P-PSDB; AAE09962.
XX      Novel polypeptides designated as NOVX polypeptides, useful in
PT      detection, prevention and treatment of e.g. Parkinson's disease and
PT      Cancer -
XX      Claim 8; Page 12; 174pp; English.
XX      The invention relates to novel G-protein coupled-receptor (GPCR) related
XX      polypeptides and their corresponding nucleotides, referred as NOVX or
XX      CC NOV1, NOV2, NOV3, NOV4, NOV5, NOV6, NOV7, NOV8, NOV9 and NOV10. NOVX and
XX      its Ab are useful for treating or preventing a NOVX-associated disorder,
XX      CC such as disorder related to cell signal processing and metabolic signal
XX      CC pathway modulation, e.g. diabetes. Pharmaceutical composition comprising
XX      CC NOVX sequence is used to treat or to prevent disorders or syndromes
XX      CC including metabolic disturbances associated with obesity, anorexia,
XX      CC wasting disorders associated with chronic diseases, infectious diseases
XX      CC (particularly infections caused by HIV-1 or HIV-2), cancer-associated
XX      CC cachexia, cancer, Parkinson's disease, Alzheimer's disease, immune
XX      CC disorders, neurodegenerative diseases and haematopoietic disorders. NOVX
XX      CC sequence is also useful for treating developmental diseases, major
XX      CC histocompatibility complex (MHC) II and III diseases (immune diseases),
XX      CC noninsulin-dependent diabetes mellitus (NIDDM), bulimia, hypotension,
XX      CC acute heart failure, multiple sclerosis, hypertension, osteoporosis,
XX      CC Crohn's disease, Alibright Hereditary Osteodystrophy, angina pectoris,
XX      CC myocardial infarction, asthma, allergies, benign prostatic hypertrophy
XX      CC and psychotic and neurological disorders, including anxiety, delirium,
XX      CC schizophrenia, manic depression, dementia, severe mental retardation,
XX      CC dentoalveopalilloalysian atrophy (DRPA) hypophosphataemic rickets,
XX      CC autosomal dominant (2) acrocallosal syndrome and dyskinisias, such as
XX      CC Huntington's disease or Gilles de la Tourette syndrome and/or other
XX      CC pathologies. NOVX DNA is used in mapping the chromosomal location of
XX      CC NOVX gene and in forensic biology. The present sequence is GPCR NOV1C
XX      CC DNA.
XX      Sequence 956 BP; 227 A; 228 C; 190 G; 311 T; 0 other;
SQ
```

```
Query Match          99.4%: Score 937.2; DB 22; Length 956;
Best Local Similarity 99.7%: Pred. NO. 3.4e-275;
Matches 939; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY      2 atgaattgggtaaatgacagcatcatcagaagattatctgcgcgggttcacagatcga 61
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```

```
Db      7 atgaattgggtaaatgacagcatcatcagaagattatctgcgcgggttcacagatcga 66
QY      62 ccttgctggagttccactccttgctgctcttgattcttccactgtagaccattc 121
        |||||||
Db      67 ccttgctggagttccactccttgctgctcttgattcttccactgtagaccattc 126
QY      122 ggaacatgacattatctagtgtagcgcctggacaccaaacttcaaccocatgtat 181
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Db      127 ggaacatgacattatctagtgtagcgcctggacaccaaacttcaaccocatgtat 186
QY      182 ttttttcccaatctatccctccttgatcttggttaaccacaatttaagttccacaa 241
        |||||||
Db      187 ttttcttaccacatcatccctccttgatcttggttaaccacaatttaagttccacaa 246
QY      242 atgctagtaaatattatgcaagcatcaggaagaatgacgtatctggtgctgtagccag 301
        |||||||
Db      247 atgctagtaaatattatgcaagcatcaggaagaatgacgtatctggtgctgtagccag 306
QY      302 ctttcatattctgacctggtgggtactggaatatcttctcgtgcgtcatgtcttc 361
        |||||||
Db      307 ctttcatattctgacctggtgggtactggaatatcttctcgtgcgtcatgtcttc 366
QY      362 gatgtgtttaggtatttgcgcctctccattaccatccagttatcgtgacacagagatc 421
        |||||||
Db      367 gatagttttaggtatttgcgcctctccattaccatccagttatcgtgacacagagatc 426
QY      422 tgcctccagttgagcagctgcatcctggttactggttttagtaactcagtggtgtct 481
        |||||||
Db      427 tgcctccagttgagcagctgcatcctggttactggttttagtaactcagtggtgtct 486
QY      482 accctgactctcagctgcatcctggttactggttttagtaactcagtggtgtgaa 541
        |||||||
Db      487 accctgactctcagctgcatcctggttactggttttagtaactcagtggtgtgaa 546
QY      542 gtccctcagctgctcagaattatctgtgtttagagacaagaatgaggtggaatttc 601
        |||||||
Db      547 gtccctcagctgctcagaattatctgtgtttagagacaagaatgaggtggaatttc 606
QY      602 ctgtcagtgagctcttccatcatatccctgacactcatccttatcatatgctttt 661
        |||||||
Db      607 ctgtcagtgagctcttccatcatatccctgacactcatccttatcatatgctttt 666
QY      662 atgttcgagagatattgagatagatcagttctgtgaaggtgacaaaagactttggaca 721
        |||||||
Db      667 atgttcgagagatattgagatagatcagttctgtgaaggtgacaaaagactttggaca 726
QY      722 tgtgttcccatcaattgtgtgtctcttttatagtagcagcgtctgtgtactgt 781
        |||||||
Db      727 tgtgttcccatcaattgtgtgtctcttttatagtagcagcgtctgtgtactgt 786
QY      782 caaccaccttgcacagctcacaagaccaaagaaagatggttctctctatgaaatc 841
        |||||||
Db      787 caaccaccttgcacagctcacaagaccaaagaaagatggttctctctatgaaatc 846
QY      842 attgacacatgctggaatcccttatatatcactttaggaacaggaagtgaagaagc 901
        |||||||
Db      847 attgacacatgctggaatcccttatatatcactttaggaacaggaagtgaagaagc 906
QY      902 tttaaaagttggttgcagaagcttcttctaacaagaataa 943
        |||||||
Db      907 tttaaaagttggttgcagaagcttcttctaacaagaataa 948
```

```
RESULT 7
AAH31669
ID      AAH31669 standard; DNA; 1071 BP.
XX
AC      AAH31669;
XX
DT      30-JUL-2001 (first entry)
XX
DE      Human olfactory receptor polynucleotide, SEQ ID NO: 242.
XX
```


KM Human: olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 XX scent profile; scent fingerprint; scent representation; ds.
 OS Homo sapiens.
 XX MO200127158-A2.
 XX 19-APR-2001.
 XX PD 06-OCT-2000; 2000MO-US27582.
 XX PF 08-OCT-1999; 99US-0158615.
 XX PR 24-FEB-2000; 2000US-0184809.
 XX PA (DIGI-) DIGISCENTS.
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 DR WPI; 2001-290713/30.
 XX New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX Claim 8; Page 273-274; 1857pp: English.
 PS The present sequence is one of a number of isolated polynucleotides
 CC which encode polypeptides involved in olfactory sensation. The
 CC polynucleotides can be used in screening for olfactory agonists and
 CC antagonists. The methods allow for the determination of primary
 CC scents and the identification of the odour receptors used to detect
 CC these primary scents. The methods also enable determination of
 CC secondary scents and the identification of combinations of odour
 CC receptors that are involved in detecting such secondary scents.
 CC This enables the construction of a scent representation (also called
 CC a scent fingerprint or scent profile), which may be used to re-create
 CC and edit scents. Libraries of olfactory receptors are useful for
 CC determining the interaction pattern of a composition with the receptors,
 CC and can be used for determining differences in the olfactory faculties
 CC of different individuals.
 XX
 XX
 SQ Sequence 1071 BP; 277 A; 248 C; 201 G; 345 T; 0 other;

Query Match 77.0%; Score 726.2; DB 22; Length 1071;
 Best Local Similarity 86.3%; Pred. No. 7e-211;
 Matches 814; Conservative 0; Mismatches 128; Indels 1; Gaps 1;
 QY 2 atgaattgggtlaaagacagcatcatcagaggttattctgtgtgttcacagatcga 61
 DB 1 atgaattgggtlaaagacagcatcagaggttattctgtgtgttcacagatcga 60
 QY 62 ccttggttgaggttcacaccccttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 121
 DB 61 ccatggtcagagatccaccccttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 120
 QY 122 ggcacatcgacatattctagtgacagcgtgcagacacacactacacccatgtat 181
 DB 121 ggcacatcgacatattctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
 QY 182 ttttttttccaactatcactctgtgacatctgtgtgtgtgtgtgtgtgtgtgtgt 241
 DB 181 ttttttttccaactatcactctgtgacatctgtgtgtgtgtgtgtgtgtgtgtgt 240
 QY 242 atgctaatgaattatgacagcatcagaagaagtaacgtatcgtgtgtgtgtgtgt 301
 DB 241 atgctaatgaattatgacagcatcagaagaagtaacgtatcgtgtgtgtgtgtgt 300
 QY 302 ctcttcataattctgtgcttggtggtggtggtggtggtggtggtggtggtggtggt 361
 DB 301 ctcttcataattctgtgcttggtggtggtggtggtggtggtggtggtggtggtggt 360

QY 362 gatgtgtttgtagctatttgcggcctccatcactacagttacatcagtcacagagatc 421
 DB 361 gatagtttgaattatttgcggcctccatcactacagttacatcagtcacagagatc 420
 QY 422 tgcctcagtttggagctgtaccccttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 481
 DB 421 tgcctcagtttggagctgtaccccttggtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
 QY 482 accctgactcctcagctgcagcactctgtgacacccatgtgtatagatcacttctctgaa 541
 DB 481 accctgacacttaagatgacacccctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 540
 QY 542 gtccctgacactgtcagatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 601
 DB 541 gtccctgacactgtcagatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
 QY 602 ctgtcagtgagctcttcacatctaatcccttgacacatccttataatgactttt 661
 DB 601 ttcacagtggtgtcattctctctaatcccttgacacatccttataatgactttt 660
 QY 662 atgtccgagcagatttgagatagacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 721
 DB 661 atgtccgagcagatttgagatagacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
 QY 722 tgtgtgtccatcattgt 781
 DB 721 tgtgtgtccatcattgt 780
 QY 782 caaccacttcgcagcactcagacaggaaggaagtggtgtgtgtgtgtgtgtgtgtgt 841
 DB 781 caaccacttcgcagcactcagacaggaaggaagtggtgtgtgtgtgtgtgtgtgtgt 840
 QY 842 atgcacacatgctgaatcccttataatatacacttgagacaggaaggaaggaagga 901
 DB 841 atgcacacatgctgaatcccttataatatacacttgagacaggaaggaaggaagga 900
 QY 902 tttaaaaggtgtgtgtgc-aagagtccttctaatacagaataa 943
 DB 901 tttaaaaggtgtgtgtgc-aagagtccttctaatacagaataa 943

RESULT 8
 ID AAH32250 standard; DNA; 1071 BP.
 XX
 XX AAH32250;
 AC
 XX
 DT 30-JUL-2001 (first entry)
 XX
 XX Human olfactory receptor polynucleotide, SEQ ID NO: 823.
 DE Human: olfactory receptor; OR; primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation; ds.
 OS Homo sapiens.
 XX MO200127158-A2.
 XX 19-APR-2001.
 XX PD 06-OCT-2000; 2000MO-US27582.
 XX PF 08-OCT-1999; 99US-0158615.
 XX PR 24-FEB-2000; 2000US-0184809.
 XX PA (DIGI-) DIGISCENTS.
 XX PA (YEDA) YEDA RES & DEV CO LTD.
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 DR WPI; 2001-290713/30.
 XX

PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 XX Claim 8; Page 508-509; 1857pp; English.
 XX
 CC The present sequence is one of a number of isolated polynucleotides
 CC which encode polypeptides involved in olfactory sensation. The
 CC polynucleotides can be used in screening for olfactory agonists and
 CC antagonists. The methods allow for the determination of primary
 CC scents and the identification of the odour receptors used to detect
 CC these primary scents. The methods also enable determination of
 CC secondary scents and the identification of combinations of odour
 CC receptors that are involved in detecting such secondary scents.
 CC This enables the construction of a scent representation (also called
 CC a scent fingerprint or scent profile), which may be used to re-create
 CC and edit scents. Libraries of olfactory receptors are useful for
 CC determining the interaction pattern of a composition with the receptors,
 CC and can be used for determining differences in the olfactory faculties
 CC of different individuals.
 XX
 XX Sequence 1071 BP; 277 A; 248 C; 201 G; 345 T; 0 other;
 SQ

Query Match 77.0%; Score 726.2; DB 22; Length 1071;
 Best Local Similarity 86.3%; Pred. No 7e-211;
 Matches 814; Conservative 0; Mismatches 128; Indels 1; Gaps 1;

QY 2 atgaattggtaaaatgacacatatacagagatttattctgctgggtttctcagatcga 61
 DB 1 atgattgggtaaaatgagtggtccacagagattcctgtagtttctcagatcga 60
 QY 62 ccttggtgagattcaccctcctggtgcttcttctgatttctcactgagacatttt 121
 DB 61 ccatggtcagatcaccctcctggtgcttcttctgatttctcactgagacatttt 120
 QY 122 ggaactgtgacacattatctagtgatcagcctgacacacaaactatccccattat 181
 DB 121 ggaactgtgacacattatcttctggtcagatggtattcaaacccacacccatgtac 180
 QY 182 tttttcttccaaatcatcaactcctcctgattctgttaccacacatgtacagccaa 241
 DB 181 tttttcttccaaatcatcaactcctcctgattctgttaccacacatgtacagccaa 240
 QY 242 atgctagtaaatatgacagatcagagaagtaacatgattatgctggtggtgacccag 301
 DB 241 atgctagtaaatatgacagatcagagaagtaacatgattatgctggtggtgacccag 300
 QY 302 ctttcaatttctgacctggtgggtgacacatcattctccctggcgcgtacgtcctt 361
 DB 301 ctttcaatttctgacctggtgggtgacacatcattctccctggcgcgtacgtcctt 360
 QY 362 gattggttgtaagctatttctgacctcctcattcattcaattatcagtcacagaagctc 421
 DB 361 gattggttgtaagctatttctgacctcctcattcattcaattatcagtcacagaagctc 420
 QY 422 tgcctcagttgagagctgacgtcctggttactggttttagtaactcaagtgtgtgtct 481
 DB 421 tgcctcagttgagagctgacgtcctggttactggttttagtaactcaagtgtgtgtct 480
 QY 482 accctgactcctcagcagcactctgtgaccccatgtgataagtaactcttctgtgaa 541
 DB 481 accctgactcctcagcagcactctgtgaccccatgtgataagtaactcttctgtgaa 540
 QY 542 gtccctgacactgaagatgacatctctgtgtgagacacagcaaatgtgggtgacatcttc 601
 DB 541 gtccctgacactgaagatgacatctctgtgtgagacacagcaaatgtgggtgacatcttc 600
 QY 602 ctgtgagtgagctcctccatcaataacccctgacactcatccttatcatatgactttt 661
 DB 601 ctgtgagtgagctcctccatcaataacccctgacactcatccttatcatatgactttt 660
 QY 662 atgtccagagcagattgagagatagcttctgtgaaggtgacaaaagacgttgggaca 721
 DB 662 atgtccagagcagattgagagatagcttctgtgaaggtgacaaaagacgttgggaca 721

DB 661 atgtccagagcagattgagagatagcttctgtgaaggtgacaaaagacgttgggaca 720
 QY 722 tgtgttcccatcctaattgtgtgtctctttttatagatcagccgtctgtgtactcg 781
 DB 721 tgtgttcccatcctaattgtgtgtgtctctttttatagatcagctatccatgtactcg 780
 QY 782 caaccacttcgcccagctcctcaggaaggaagatgtgttcttcttctatgtatc 841
 DB 781 caaccacttcagccagctcctcaggaaggaagatgtgttcttcttctgtgatac 840
 QY 842 atgtccacactgtcgaatcccttatatacacttagaagacagaggtaaaggaagc 901
 DB 841 atgtccacactgtcgaatcccttatatacacttagaagacagaggtaaaggaagc 900
 QY 902 tttaaaagttggttc-aagagcttcttataatcaagaataa 943
 DB 901 tttaaaagttggttc-aagagcttcttataatcaagaataa 943

RESULT 9
 AAH32231 ID AAH32231 standard; DNA; 648 BP.
 XX
 AC AAH32231;
 XX
 DT 30-JUL-2001 (first entry)
 XX
 DE Human olfactory receptor polynucleotide, SEQ ID NO: 804.
 XX
 KW Human; olfactory receptor; OR: primary scent determination;
 KW secondary scent determination; polypeptide library; odour receptor;
 KW scent profile; scent fingerprint; scent representation; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200127158-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 06-OCR-2000; 2000MO-US27582.
 XX
 PR 08-OCR-1999; 99US-0158615.
 PR 24-FEB-2000; 2000US-0184809.
 XX
 PA (DIGI-) DIGISCENTS.
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
 XX
 DR WPI; 2001-290713/30.
 XX
 XX
 PT New polynucleotides which encode polypeptides involved in olfactory
 PT sensation for identifying olfactory agonists and antagonists -
 XX
 XX Claim 8; Page 502; 1857pp; English.
 XX
 CC The present sequence is one of a number of isolated polynucleotides
 CC which encode polypeptides involved in olfactory sensation. The
 CC polynucleotides can be used in screening for olfactory agonists and
 CC antagonists. The methods allow for the determination of primary
 CC scents and the identification of the odour receptors used to detect
 CC secondary scents. The methods also enable determination of
 CC secondary scents and the identification of combinations of odour
 CC receptors that are involved in detecting such secondary scents.
 CC This enables the construction of a scent representation (also called
 CC a scent fingerprint or scent profile), which may be used to re-create
 CC and edit scents. Libraries of olfactory receptors are useful for
 CC determining the interaction pattern of a composition with the receptors,
 CC and can be used for determining differences in the olfactory faculties
 CC of different individuals.
 XX
 XX Sequence 648 BP; 144 A; 166 C; 132 G; 206 T; 0 other;

Query Match 68.0%; Score 641.6; DB 22; Length 648;
 Best Local Similarity 99.4%; Pred. No. 3,4e-185;
 Matches 644; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 203 ctcttgatcttcttaccacatgtacagctcccaaatgtcagaattatgcagc 262
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 Db 1 ctcttgatcttcttaccacatgtacagctcccaaatgtcagaattatgcagc 60
 QY 263 atcaggaagaatcagttacgtgctgtgtagccagcttcatattcttcgctg 322
 |||||||
 Db 61 atcaggaagaatcagttacgtgctgtgtagccagcttcatattcttcgctg 120
 QY 323 ggggactaatactctctcgcgtcagctgcttctgtatgtttgtatgtatgt 382
 |||||||
 Db 121 ggggactaatactctctcgcgtcagctgcttctgtatgtttgtatgtatgt 180
 QY 383 cggcctcctacatcctacgtatcatatgcacagagactgtcctcagctgtgca 442
 |||||||
 Db 181 cggcctcctacatcctacgtatcatatgcacagagactgtcctcagctgtgca 240
 QY 443 tccgtggttactgttttaagtaactggtgtgtgtctacccgtacgtctcagctgca 502
 |||||||
 Db 241 tccgtggttactgttttaagtaactggtgtgtgtctacccgtacgtctcagctgca 300
 QY 503 ctctgtgacccctatgtgatcacttctcgtgaaagtcctgtcagctgtcaagtt 562
 |||||||
 Db 301 ctctgtgacccctatgtgatcacttctcgtgaaagtcctgtcagctgtcaagtt 360
 QY 563 tctgtgttggagaagaagaatgaggtgagactatctctgtcagtgagcttccat 622
 |||||||
 Db 361 tctgtgttggagaagaagaatgaggtgagactatctctgtcagtgagcttccat 420
 QY 623 ctaataccctgtgacacatcctatcatatcatgtcttattgttcgagcgatagag 682
 |||||||
 Db 421 ctaataccctgtgacacatcctatcatatcatgtcttattgttcgagcgatagag 480
 QY 683 ataatgctgctgaggtgtgacaaaagcatcttgagacatgtgttcccatcaattgtg 742
 |||||||
 Db 481 ataatgctgctgaggtgtgacaaaagcatcttgagacatgtgttcccatcaattgtg 540
 QY 743 gtgtcctttttttatagacagcgctctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 802
 |||||||
 Db 541 gtgtcctttttttatagacagcgctctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
 QY 803 aaggaaccaagaaagatgttctctctcttcatgtgaatcattgcacc 850
 |||||||
 Db 601 aaggaaccaagaaagatgttctctctcttcatgtgaatcattgcacc 648

RESULT 10
 AAC77475
 ID AAC77475 standard; cDNA; 1442 BP.
 XX AAC77475:
 AC
 XX
 DT 08-FEB-2001 (first entry)
 DE
 XX
 XX
 Human ORFX ORF3030 polynucleotide sequence SEQ ID NO: 6059.
 Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;
 KM vulnary; antiproliferative; antiparkinsonian; neuroprotective;
 KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KM hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KM antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KM antineoplastic; gene therapy; cancer; proliferative disorder; hypertension;
 KM neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KM cholesterol ester storage; systemic lupus erythematosus; infection;
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;

KW thrombosis; contraceptive; ss.
 XX
 OS Homo sapiens.
 XX
 XX W0200058473-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000MO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2000-602362/57.
 DR P-PSDB; ABA3266.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 5; Page 5245-5246; 5507Pp; English.

XX AAC74446 to AAC77606 encode the proteins given in ABA40237 to ABA43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antiproliferative; antiparkinsonian; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antineoplastic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 XX
 SQ Sequence 1442 BP; 378 A; 319 C; 268 G; 477 T; 0 other;

Query Match 56.6%; Score 534; DB 21; Length 1442;
 Best Local Similarity 72.9%; Pred. No. 3e-152;
 Matches 687; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 2 atgaattggtaaatgacagcatcatcagaggttattctgtcgtggttcttcagatcga 61
 |||||||
 Db 301 atgaattggtaaatgacagcatcatcagaggttattctgtcgtggttcttcagatcga 360
 QY 62 ccttgctgaggttccacccctgtgttcttctgttcttcttcaactgtgacatcttc 121
 |||||||
 Db 361 gcttggttaacaaagcccttctgtgtctctttaaatacatcacacacacatctt 420
 QY 122 ggcacatggacatcttctagttcagcgctgtgacacaaacttaccacacatgtat 181
 |||||||
 Db 421 ggcacatggacatcttctagttcagcgctgtgacacaaacttaccacacatgtat 480
 QY 182 ttcttctacatcatcactcctgtgactcttgttatacacaatgtatagtcacaa 241
 |||||||
 Db 481 ttcttctacatcatcactcctgtgactcttgttatacacaatgtatagtcacaa 540

OY	242	atgtatagtaaatattatgcaagcatcaggaagaatcaacagttatcgtgtgctgtgtgacccag	301
Db	541	atgtttgttaataatttgtttgttcaacaaaagaccacacagcatatgtcgtgtgtgtgtccac	600
OY	302	cttttcataatttcggcctctgagggtcaatgtataatctctccctgtgcgcgtcatctctt	361
Db	601	ctcaatactctcctgtgcccaggtgtctaaagggtgtctcctctcgtgcgtgtatgtcctt	660
OY	362	gattgtgtttgtagcatattgttcggcctctccatactcaatgthalcagaccagaagactc	421
Db	661	gacagataatgtgtctttgttcagagcccccacacatgtatgcatcatgaattatgttct	720
OY	422	tgtccacagttgtcagctgataccctgcctgtgttaattgttttagaacatagttgtgtgct	481
Db	721	tgtctaagatgtgtcagcctctccatcctcatgtcctatgtttcttcggacaacctcaggtctcagact	780
OY	482	accctgaactctcagctcagctcagctctgtgaaccctatgtatagatcaacttctctgtga	541
Db	781	tccttgcctcttaacaatgcaacgctgtgtgttcacaggaagtgagcacctcttctctgtag	840
OY	542	gtcccctgactgttcagatattcttgtttgttgacaacacggaatgagctggaactatc	601
Db	841	gtgcgcgcactcttcgaattgtgtcagatgtgtgtgcacacaagccatattgaagcgcgaactctc	900
OY	602	ctgttcagtgagctctctcattcaatcaatacaccgcggacaactatctatatactgacttt	661
Db	901	ttctttagtgtactaatctcttcaattccagtcaggaatgattcctcatctctatgtcttc	960
OY	662	atgttcgagcagatatttgtagatagacagctgtgtgttgatgtgcacaaaagacatttgggaca	721
Db	961	atagcctcaagcagatatttaaaaaaatacaggtccagacaagaagcgcggcacaanaagcatcttgggaca	1020
OY	722	tgtgtgtccacatcaattgtgtgtgtctcttcttctttagtacagcgcgtctcgttacctg	781
Db	1021	tgtgtgtccacatgattgtgtgtgtcctctctttagtagaagcgcattatatagtactt	1080
OY	782	caaccaccttcgcccagctctccaaaggacccaagaagaatgtgttctctctcttataggaaac	841
Db	1081	caaacaccttcaatccacactcctaagagacgtgggagaagaatgtgttctctcttcatatgaaac	1140
OY	842	atttcaccccatctgtgaataccctctatataataacttagtaacaaagaggtlaaagaagc	901
Db	1141	atcacatcatcatgttgtaactctccctcatctcagccttagagaataaagatatgaaggagcc	1200
OY	902	tttaaaaggttgtgttcgaagatctcttctaataccaagaataa	943
Db	1201	ttcaagagctgtatgcacaagaatctttcttctgtagaataa	1242

	RESULT	11
AAH32304		
ID	AAH32304	standard; DNA; 939 BP.
XX		
AC		
XX	AAH32304;	
DT		
XX	30-JUL-2001	(first entry)
DE		
XX	Human olfactory receptor polynucleotide, SEQ ID NO: 877.	
XX		
KW	Human; olfactory receptor; OR; primary scent determination;	
KW	secondary scent determination; polypeptide library; odour receptor	
KW	scent profile; scent fingerprint; scent representation; ds.	
XX		
OS	Homo sapiens.	
XX		
PN	W0200127158-A2.	
XX		
PD	19-APR-2001.	
XX		
PF	06-OCT-2000; 2000MO-US27582.	
XX		
PR	08-OCT-1999; 99US-0158615.	
PR	24-FEB-2000; 2000US-0184809.	

XX	(DIGI-) DIGISCENTS.
PA	(YEDA) YEDA RES & DEV CO LTD.
XX	
PI	Bellenson J, Smith D, Lancel D, Glusman G, Fuchs T, Yanai I;
DR	WPI; 2001-290713/30.
XX	
PT	New polynucleotides which encode polypeptides involved in olfactory
PT	sensation for identifying olfactory agonists and antagonists -
XX	
PS	Claim 8; Page 530; 1857pp; English.
XX	
CC	The present sequence is one of a number of isolated polynucleotides
CC	which encode polypeptides involved in olfactory sensation. The
CC	polynucleotides can be used in screening for olfactory agonists and
CC	antagonists. The methods allow for the determination of primary
CC	scents and the identification of the odour receptors used to detect
CC	these primary scents. The methods also enable determination of
CC	secondary scents and the identification of combinations of odour
CC	receptors that are involved in detecting such secondary scents.
CC	This enables the construction of a scent representation (also called
CC	a scent fingerprint or scent profile), which may be used to re-create
CC	and edit scents. Libraries of olfactory receptors are useful for
CC	determining the interaction pattern of a composition with the receptors
CC	and can be used for determining differences in the olfactory faculties
CC	of different individuals.
XX	
SO	Sequence 939 BP; 232 A; 228 G; 185 G; 294 T; 0 other;

[illegible]

D	b	541	gugccgcagcattctcaagtgtgtcatgtgtcgacacaagaacctatgtgaaggctgagctcttc	600
O	y	602	cttgcacagtgagcgtctccatccataaccctcgacactcatccattatatcatatgtcttt	661
D	b	601	tctcttagtgcactaatctctcttatccaaagtgcacattgatctcctctcctatgtgttc	660
O	y	662	attgtccgagcagatattgaggatcacagtcgtctgaagtcgcacaaaaagcatttgggaca	721
D	b	661	atagtcacagcagatataaaaatcagtcgaagcagaagacgcgcaaaaagcatttggaca	720
O	y	722	tgtgttcccattccaatttgtgtgtctcttttttatagtcaacgcgtctctgtgacccy	781
D	b	721	tgtgtgtccccacgattgtgtgtgtctctctttatttgaacaagccatttatatgtatctt	780
O	y	782	caaacacccttgcgcagctccaaaggaccaaaggaaagtgtttctctctctatgtgaac	841
D	b	781	caaccaccttataccacaccttaagagcttgggaaagtgtttccctctctatgtgaatc	840
O	y	842	attgcaccacatgtcgtgaatccctctatalatacactttagagacaaggatftaaagaaagc	901
D	b	841	atcacatccatgttgtaacctccctcatctacagccttagaataagatatagaaggagcc	900
O	y	902	tttaaagaattgtgttcgaagaagcttcttbatcaagaag	940
D	b	901	ttaagaagcgtgcagtcacagatcttcttcttgaagaag	939

RESULT	12
AA542221	
ID	AA542221 standard; cDNA; 939 BP.
XX	
AC	
XX	AA542221;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Human cDNA encoding olfactory receptor AOLFRI3.
XX	
KW	Human; olfactory receptor; G protein-coupled receptor; GPCR; odourant;
XX	ss; food additive; cosmetic; fragrance; pharmaceutical additive.
XX	
OS	Homo sapiens.
XX	
PN	WO200168805-A2.
XX	
PD	20-SEP-2001.
XX	
PF	13-MAR-2001; 2001WO-US07771.
XX	
PR	13-MAR-2000; 2000US-018914.
PR	24-MAR-2000; 2000US-0192033.
PR	12-APR-2000; 2000US-0198474.
PR	24-APR-2000; 2000US-0199335.
PR	26-MAY-2000; 2000US-0207702.
PR	23-JUN-2000; 2000US-0213849.
PR	16-AUG-2000; 2000US-0226534.
PR	07-SEP-2000; 2000US-0230732.
PR	07-FEB-2001; 2001US-0268662.
XX	
PA	(SENO-) SENOMYX INC.
XX	
PI	Zozulya S;
XX	
DR	WPI: 2001-570867/64.
XX	
DR	P-PsDB; AAU24528.
XX	
PT	Nucleic acids encoding human olfactory G protein-coupled receptors,
XX	useful for screening for compounds involved in olfactory sensation,
XX	where the compounds can be used in the food, pharmaceutical and
XX	cosmetic industries to customise odours -
XX	
PS	Claim 1; Page 89; 31ppp; English.
XX	
CC	The invention relates to nucleic acids encoding human olfactory

receptors, OR, (a G protein-coupled receptor, GPCR). The OR's specifically recognise molecules, odourants, that elicit specific olfactory sensation. The human olfactory receptors and polynucleotides encoding them are useful for screening a library of chemical compounds for compounds that are involved in olfactory sensation. Modulators of their activity are useful for pharmacological and genetic modulation of olfactory signalling pathways. Therefore, they can be used in the food, pharmaceutical and cosmetic industries to customise odours and fragrances. The present sequence encodes a human olfactory receptor of the invention.

Sequence 939 BP; 223 A; 227 C; 190 G; 298 T; 1 other;

Query Match	42.8%	Score 403.6;	DB 22;	Length 939;
Best Local Similarity	65.1%;	Pred. No. 1.3e-112;		
Matches 595; Conservative	0;	Mismatches 319;	Indels 0;	Gaps 0

OY	2	atgaatctggtataatgacagcatcatacagagattatctctgctgtgtcttcacatgca	61
Db	1	atgagatcagaaaaatggaagctctctcaatctgattatctactctgggtcttcctgaag	60
OY	62	octtgctgagtgatctccaaactcctctgtgtcctctctgattctctaacacgtgacatcctt	121
Db	61	octcaagctggagactgctcctcttctgtgtctcttttgatctctatactctcaatttgcgt	120
OY	122	ggcaactctgacatattctctagtgatcagcctctgacacccaactcctaaccctccatg	181
Db	121	gggaacaaaacacatcatctgtattatctcactctggaccacatctcacaatccatg	180
OY	182	ttttcttctcaaatctatcactcctctgtaacttttctgtttaaacaatgtcagctccacaa	241
Db	181	ttttctctctcccaacaaactaagcctctcttgactctgtgttaaacaacaggcaactctccacag	240
OY	242	atgcagctgaataattatgcagcatcagagaagtaacagtaactatcgtgtcgtgttaagccag	301
Db	241	ctctcgtgttaatctcagggagcagacaataatcctcctatgtatgtgtgtgttaag	300
OY	302	ctttccatattctctgctccttgggtggtactatgtaatactctctccctggccgtcatgtccctt	361
Db	301	ctgtacatctctcctagcgtcttggagctacaagaatgcgtctctcttaaggatgtatgacatt	360
OY	362	gattggttctgatactatttctgtcgcgcctcccaattactcaagtataatgacacagagact	421
Db	361	gacgcgtatgcagcctgttttgacagccctccacatacaacagtatgatacctctgtcctg	420
OY	422	tgcctcagctgtgcagctctgacatccctgtggttactggttttagtaactcagtggtgtgct	481
Db	421	tatgtctgatagtctctactctcaatctgagtcattgtgttttgcaacactccctatctgcagag	480
OY	482	accctgacatctccagctgcacatcctctgtgagacccctcttgatagatgacacttctctgtga	541
Db	481	gtgcacatctgtctttaaactctgtgtggaagaataaataatgagaacacttctctgtgtgag	540
OY	542	gtccctctgacatctcaagttactctgtctgttgagacaacagacgaagctgataactact	601
Db	541	gtctctcatctgtcctaagctgtccgtgtgtgtgacactactatgataatgaaatctgaactcttc	600
OY	602	ctgtcagtgagctcttccatctaataaccctgtgacatcatcccttatatcatatgcttct	661
Db	601	tttgcagtgatcatattctctcttcttactcgtgtgcatatcatatcttccctatgtcag	660
OY	662	attgctccgacagtatcttgagataacagttcgtgtgaagttcgacaaaagcatttgggaca	721
Db	661	attgtcagaaggacgtctgtgagataaagatcagaacacagggcagagaagaatgttcttgggaca	720
OY	722	tgtgtgtccacataattgtgtgtctctctttaaataagacgcgcgtctgtgtgacgt	781
Db	721	tgtgtctccacactcaacgtgtgtcttccctgttctcagcgacagcgtatctatgtctaactc	780
OY	782	caacacactctgcgccagctctccaagacgaagaaagatgtttctctctcttaatgaaatc	841
Db	781	caaccccggaacaactactctcagagatacaggaagqktaactctctctcttcaacatc	840

KM cerebroprotective; G-coupled receptor; cell proliferative disease;
KM lymphoma; leukaemia; breast cancer; cirrhosis; neurological disorder;
stroke; Alzheimer's disease; multiple sclerosis; mental retardation;
KM cardiovascular disease; atherosclerosis; angina pectoris; indigestion;
KM congestive heart failure; gastrointestinal disorder; dysphagia; AIDS;
KM gastritis; autoimmune disorder; inflammatory disorder; Crohn's disease;
KM systemic lupus erythematosus; metabolic disorder; diabetes; obesity;
KM viral infection; herpesvirus; parvovirus;
KM acquired immune deficiency syndrome; ss.

OS Homo sapiens.

PN W0200190359-A2.

PD 29-NOV-2001.

PF 22-MAY-2001; 2001WO-US16833.

PR 22-MAY-2000; 2000US-206222P.

PR 02-JUN-2000; 2000US-208834P.

PR 07-JUN-2000; 2000US-209868P.

PA (INCY-) INCYTE GENOMICS INC.
XX

PI Patterson C, Tribouley CM,
Wallerstein J, Gershoff E, & Tjebk

XX WPT, 2003-106100/14
DB

DR P-PSDB; AAU80497.
YY

PT	New G-protein coupled receptor
BT	proliferation (G-protein coupled)

PT	cardiovascular or autoimmune
YY	

PS Claim 5; Page 140; 148pp; En
XY

CC The invention relates to a method for determining the

CC preventing cell proliferative diseases (e.g. lymphoma, leukemia, breast
CC cancer or cirrhosis), neurological disorders (e.g. stroke, Alzheimer's
CC disease, multiple sclerosis or mental retardation), cardiovascular
CC diseases (e.g. atherosclerosis, angina pectoris or congestive heart
CC failure), gastrointestinal disorders (e.g. dysphagia, indigestion or
CC gastritis), autoimmune/inflammatory disorders (e.g. AIDS, Crohn's disease
CC or systemic lupus erythematosus) or metabolic disorders (e.g. diabetes
CC or obesity), or viral infections (e.g. infection by herpesvirus or
CC parvovirus). ARI1615-ARI1637 represent novel human G-coupled
CC receptor coding sequences of the invention.

SQ Sequence 939 BP; 223 A; 226 C; 189 G; 301 T; 0 other;

Query Match	42.6%	Score 402	DB 24	Length 939
Best Local Similarity	65.0%	Pred. No.	4.1e-112	
Matches 594	Conservative	0	Mismatches 320	Indels 0
				Gaps 0

QY	2	atgaattgaggaaatgacagatcatatcaaggagttattctgcgtgttctcaatcga	61
	1	atggatccagaaaaatctgaaagttctcttcaactggaattatcctcaacgggttctctcgaaagg	60
Db			
QY	62	ccttgctgagagttccatcctcctgtgctctctgtattctctcaactgtgacatcttt	121
	111	1111111	1111111
Db	61	cctcagctcgagagctagcctccttgggtgtcttctgtactctatcatcctaacttgcgtg	120
QY	122	ggcaatctgacattatcttagtgtcagcgcctcgacaaccaacttcaaccoccatgtat	181
	111	1111111	1111111
Db	121	gggacacaaaacatcatctgtattatctccacttggacccacatcttcaactctcatgtat	180
QY	182	ttttcttaccaatatcatcctcctctgatactcttgtaaccacaaatgataagcctccaaa	241
	1111111	1111111	1111111
Db	181	ttttctctctcaacacaaagcttttttgagactcgtgttaacaaacacggcatctgttccacag	240

QY	242	atgctagtaagaatattatgcagcatccaggaagtatgcgtatgctgtgtgagccag	301
Db	241	ctccctggttaactcctaaggggagcagcaacaataactctccatctgtgtgtgttcag	3000
QY	302	ctttccatattctctgcccctgggggctactgaatactctcccgccgcatctccctt	361
Db	301	ctgtacatctctctcagctgtggatccatccagaatgcygtctctcttagagtgatattc	3600
QY	362	gattgtgtttgtagctattttgcgggcctctccattaccatccagtatcatcagcaccagaactc	4221
Db	361	gaccgctatgcagctgttttgagggccctccacacacagtagtcatcagcccttgcg	4200
QY	422	tgcgcccaagttagcagcgcgcatccctgggtttacgtgttttaagtaacatggtgtgtctc	481
Db	421	tatgtgcgtagtgctctcactactcaatgggtcaattgttttgccaactcccatgtgcagcg	480
QY	482	accctgactctccagctgcgcacactctgtgacccctatgtatagatcaactctctgtgaa	5411
Db	481	gtccacactctgtcttttaacactctgtgtgaaagaataatagaacactctcttctgtag	5400
QY	542	gtccctgcacgtcctaagttactctgtgtgttagaacaacagcaaatgaggtgcgaactctc	6010
Db	541	gtctccatctgtcttaagacttgcgcgtgtgtgaacactactaagaatgaatctgcgaactcttc	6000
QY	602	cttctgcagtgcctctctccatctaataccctgcgaactcatcccttatatacatatgctcttc	661
Db	601	tttgcacgtgtcatatctctctctgttaccttctgtcatatacatatctccctatagtcag	6600
QY	662	attgtgcgagcagtatctagagatacagctcgtcgaagctgcacaanaagcattgttgaca	721
Db	661	attgtccagggcagctatcagagataaagttagcaacacgggcagcaaaaagtgtttgaca	7200
QY	722	tgtgtgtcccatctaattgtgtgtctctcttttatagtacagcgcgtctcgtgtacctg	781
Db	721	tgtgtgtcccaactacagtgcttctccctgttctacggccaagctatcatatgcttacctc	7800
QY	782	caacacactctgcgcagctcccaaggacccaaggaagatgtgtctctctctatgagatc	8411
Db	781	cagcccggaacaatactctccagatcagtaaggcaagtcatatctctctctctaacacatc	8400
QY	842	attgcacacatgtgtaactccctctatatcatatcactttagaacaagggaggtlaaaggaagc	901
Db	841	attacacccatgatcaaacccctcatatatatacacttgagggaacagagtgtagaagggca	9000
QY	902	tttaaaagtttgt	915
Db	901	cttaagaagtgct	914

RESULT 15

ID	AAH32063	standard; DNA; 1002 BP
1	ATG	1
2	ATG	2
3	ATG	3
4	ATG	4
5	ATG	5
6	ATG	6
7	ATG	7
8	ATG	8
9	ATG	9
10	ATG	10
11	ATG	11
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122	ATG	122
123	ATG	123
124	ATG	124
125	ATG	125
126	ATG	126
127	ATG	127
128	ATG	128
129	ATG	129

AC AAH32063;

DT 30-JUL-2001 (first entry)

DE Human olfactory receptor polynucleotide, SEQ ID NO: 636.

KW Human; olfactory receptor; OR; primary scent determination;

KW scent profile; scent fingerprint; scent representation; ds.

05 Homo sapiens.

PN W0200127158-A2.

PD 19-APR-2001.

PF 06-OCT-2000; 2000WO-US27582.

PR 08-OCT-1999; 99US-0158615.

PR 24-FEB-2000; 2000US-0184809.

PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Belenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;

DR WPI; 2001-290713/30.

PT New polynucleotides which encode polypeptides involved in olfactory sensation for identifying olfactory agonists and antagonists -

PS Claim 8; Page 435-436; 1857pp; English.

CC The pre-sequence is one of a number of isolated polynucleotides
CC which encode polypeptides involved in olfactory sensation. The
CC polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary
CC scents and the identification of the odour receptors used to detect
CC these primary scents. The methods also enable determination of
CC secondary scents and the identification of combinations of odour
CC receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called
CC a scent fingerprint or scent profile), which may be used to re-create
CC and edit scents. Libraries of olfactory receptors are useful for
CC determining the interaction pattern of a composition with the receptors,
CC and can be used for determining differences in the olfactory faculties
CC of different individuals.

SQ Sequence 1002 BP; 210 A; 266 C; 217 G; 309 T; 0 other;

Query Match 39.48; Score 371.6; DB 22; Length 1002;

Best Local Similarity 62.5%; Pred. No. 7.8e-103;

Matches 581; Conservative 0; Mismatches 349; Indels 0; Gaps 0;

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OY	254	ttatgcagcatcagaagaagtaatcagttatcgtggtctgtgtagccagcttttccaatlt	313
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OY	314	cttgcgttggtgggtcattgaatactctctccctgcgtcaatgttccctttgattgtttga	373
Db	373	catgcctctggatcatccaactgtagtgcctcccggtctgtgatctcctgtgtgacgcgtatgtg	432
OY	374	gcatatttgcgcctctccatctacatcaagtatactatgcacacagaaactctgcctccagttg	433
Db	433	gctgtctgcgtctctctccatctacatcgtcttactatgatataccaactctctgcatgacctg	492
OY	434	gcagctgcataccctggttactggttttaagtaactcagtgctgtgtctacacctgactcc	493
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Qy 614 ctcttcataataacccctgacacatcattcattatcatatgctttattgctcgagca 6733

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Search completed: August 25, 2002, 19:02:13
Job time: 4201 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 17:41:07 : Search time 77.06 Seconds
(without alignments)
3005.871 Million cell updates/sec

Title: US-09-800-321A-3

Perfect score: 943

Sequence: 1 tatgaatggtgaataagca.....tcttctaataagaataaa 943

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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6: /cgn2_6/ptodata/2/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	215.2	22.8	1290	2 US-08-827-291A-1	Sequence 1, Appl
2	213.2	22.6	966	3 US-08-748-506-7	Sequence 7, Appl
3	212.6	22.5	966	3 US-08-748-506-8	Sequence 8, Appl
4	201.6	21.4	900	4 US-09-085-371-5	Sequence 5, Appl
5	199.2	21.1	1713	2 US-08-467-948A-1	Sequence 1, Appl
6	199.2	21.1	1713	3 US-08-467-947A-1	Sequence 1, Appl
7	198.8	21.1	966	3 US-08-748-506-5	Sequence 5, Appl
8	192	20.4	966	3 US-08-748-506-6	Sequence 6, Appl
9	185.2	19.6	984	3 US-08-748-506-9	Sequence 9, Appl
10	120	12.7	963	4 US-09-439-313-526	Sequence 526, App
11	116.8	12.4	1474	1 US-08-465-980-1	Sequence 1, Appl
12	116.8	12.4	1474	1 US-09-053-303-1	Sequence 1, Appl
13	116.8	12.4	1474	5 PCT-US95-07093-1	Sequence 1, Appl
14	96	10.2	1828	3 US-08-988-876-2	Sequence 2, Appl
15	90.2	9.6	1320	1 US-08-599-352-84	Sequence 84, Appl
16	90.2	9.6	1320	1 US-08-436-074-57	Sequence 57, Appl
17	90.2	9.6	1320	5 PCT-US96-06352-84	Sequence 84, Appl
18	90.2	9.6	1320	5 PCT-US96-06583-84	Sequence 84, Appl
19	59	6.3	7218	1 US-08-232-463-14	Sequence 14, Appl
20	41.6	4.4	1137	3 US-09-082-088-1	Sequence 1, Appl
21	41.6	4.4	1137	4 US-09-546-117-1	Sequence 1, Appl
22	41.4	4.4	1260	1 US-08-599-352-83	Sequence 83, Appl
23	41.4	4.4	1260	1 US-08-436-074-56	Sequence 56, Appl
24	41.4	4.4	1260	5 PCT-US96-06352-83	Sequence 83, Appl
25	41.4	4.4	1260	5 PCT-US96-06583-83	Sequence 83, Appl
26	39.8	4.2	2012	3 US-08-706-281A-7	Sequence 7, Appl
27	39.8	4.2	2012	4 US-09-097-231-7	Sequence 7, Appl

C	28	37	3.9	251	4	US-09-439-313-352	Sequence 352, App
	29	36.6	3.9	1015	1	US-08-671-525B-3	Sequence 3, Appl
	30	36.6	3.9	1015	1	US-08-672-109B-3	Sequence 3, Appl
	31	36.6	3.9	1015	1	US-08-842-045-3	Sequence 3, Appl
	32	36.6	3.9	1015	2	US-08-842-238-3	Sequence 3, Appl
	33	36.6	3.9	1015	3	US-08-629-335B-3	Sequence 3, Appl
	34	36.6	3.9	1015	3	US-07-866-560-3	Sequence 3, Appl
	35	36.6	3.9	1012	1	US-08-077-673-3	Sequence 3, Appl
	36	36.6	3.9	1012	1	US-08-478-992-3	Sequence 3, Appl
	37	36.6	3.9	1012	3	US-09-105-298-3	Sequence 3, Appl
C	38	34	3.6	289	4	US-09-007-005-17	Sequence 17, Appl
C	39	34	3.6	289	4	US-09-244-796-17	Sequence 17, Appl
C	40	31.8	3.4	1101	3	US-08-945-056-5	Sequence 5, Appl
C	41	30.8	3.3	753	4	US-08-998-416-574	Sequence 4, App
C	42	30.4	3.2	603	3	US-08-609-334-10	Sequence 10, Appl
C	43	30.4	3.2	603	3	US-08-609-334-15	Sequence 15, Appl
C	44	30.4	3.2	1092	4	US-09-077-675A-15	Sequence 15, Appl
	45	30.4	3.2	3129	4	US-09-077-675A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-827-291A-1
Sequence 1, Application US/08827291A
Patent No. 5874243
GENERAL INFORMATION:
APPLICANT: Macina, Roberto
TITLE OF INVENTION: NOVEL OLRCC15 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smltkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: PA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: King, William T
REGISTRATION NUMBER: 30,954
REFERENCE/DOCKET NUMBER: GP50001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-827-291A-1

Query Match 22.8%; Score 215.2; DB 2; Length 1290;
Best Local Similarity 52.1%; Pred. No. 1.9e-57;
Matches 481; Conservative 0; Mismatches 443; Indels 0; Gaps 0;

OY	2	atgaatttggcgaataagcaagatcatcacaggagttaattctgtggtttccaaagtcga	61
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OY	62	ccttgctcgtagttccaactcctctgtgtctctcttgaattctctaacttgacaacttt	121
Db	356	AGCCCCAACCCACACCTTCCTCTTCTTGCTGTCTCGGCCAATCTTTTCAGGGCCTTCAG	415
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Db	416	GGAACAATCTGTCAAGTGTCTCTCATCTACCTGGACACCAGCTCCACACCCCACATGTAC	475
OY	182	tttttcttaccaatatcataactccttgaccttttgttaaaccacatgtaagttcccaca	241
Db	476	CTTCCTCTACCCAACTAGTCTCCTATAGGACCTATGCTCATTTGCACACCACCGTACCAAG	535
OY	242	atgcataagaaatttatgcaagatcatcaagaagaagtaatacagttatcgltgtgtgaagccag	301
Db	536	ATGGCCTTCAACATCACTGCTCGGAGAGAATACTTTCATTTGGCTGTGTGTGCGACACNA	595
OY	302	ctttacabattcttgsccttgagggtcactgaatalctctccgtgcgtcatgtccctt	361
Db	596	ATTTCCTCTTAATCATCACTGCTGTGCTGTGAATGCTTTCTTTGGCTGTATAGGCTTAT	655
OY	362	gattggttttagaglatatttltggtccctccatctaacctagttatcatatgacaagagacc	421
Db	656	GACCGCTAACACTGGCAATTTGGCAACCCCTCTTAGATATACCAACATCTCATGTAGGCCCTTAAAT	715
OY	422	tgcctccagttgcagcgtcgaactccgttggttaactcgttttgtaactcagtggtgtct	481
Db	716	TGTGACTTATGACTGTGCTTTTCTGTGATTCCTGTGGCTCTAGAGATGGAAATCATTTATGCT	775
OY	482	aacctgactctcagactgtgcaactctgtgacccctaigtatagatcaacttccctgtgaa	541
Db	776	GTAGGACAAATTTTCCTTCTCTACTGTGTGGGTCTCGGGAAATATAGCCCATCTTCTGTGAG	835
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Db	896	ATTGTGCTCTATAGTAATGTCTTGTCTTCCCTGTGTGCATCATCTATTCCTTCTCTATGTGGA	955
OY	662	atgtccgaagcaglatitgaagatacagctctgtcgaaggtcgacaanaaagcatitvggaca	721
Db	956	GTTATTTGCTGTCTCATTTCAATGAGATCTGAGAGAGGGTGTGCGCAAACTTTTACAGACC	1015
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OY	782	caaccacaccttcgccagcgtcccaagyaaccaagaagaatgtgtctctctctcatggaatc	841
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RESULT 2
 US-08-748-506-7
 : Sequence No., Application US/08748506
 : Patent No. 6159707
 : GENERAL INFORMATION:
 : APPLICANT: Ronnett et al.
 : TITLE OF INVENTION: NOVEL SPERM RECEPTORS
 : NUMBER OF SEQUENCES: 31

```

1 CORRESPONDENCE ADDRESS:
2 ADDRESSEE: Ievdly, Voit & Mayer, Ltd.
3 STREET: Two Prudential Plaza, Suite 4900
4 CITY: Chicago
5 STATE: IL
6 COUNTRY: US
7 ZIP: 60601-6780
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patentln Release #1.0, Version #1.25
13 CURRENT APPLICATION DATA:
14 APPLICATION NUMBER: US/08/748,506
15 FILING DATE: 08-NOV-1996
16 CLASSIFICATION: 435
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US 60/033,751
19 FILING DATE: 09-NOV-1995
20 CLASSIFICATION: 435
21 ATTORNEY/AGENT INFORMATION:
22 REFERENCE/DOCKET NUMBER: 74940
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 312-616-5600
25 TELEFAX: 312-616-5700
26 INFORMATION FOR SEQ ID NO: 7:
27 SEQUENCE CHARACTERISTICS:
28 LENGTH: 966 base pairs
29 TYPE: nucleic acid
30 STRANDEDNESS: double
31 TOPOLOGY: linear
32 MOLECULE TYPE: DNA (genomic)
33 US-08-748-506-7

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Query Match	22.68;	Score 213.2;	DB: 3;	Length 966;
Best Local Similarity	55.48;	Pred. No. 6.9e-57;		
Matches 413;	Conservative	0;	Mismatches 333;	Indels 0;
				Gaps 0;
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OY 224	acatgtacagtcgccacaatgtctagtaaatatgatgcagacaggaagaatcatagttat	283		
Db 241	TGCTCTGTGCATACCCCAACATGCTGCAGAGCCCTTGTGATGTGAGGCCCGAGGGATCTTTGG	300		
OY 284	cgctgctgtgtacgcagcttccatattcttcgacctggtgggactgaatcatctctc	343		
Db 301	GAGGTTGTGGCTCAGACATGTCTCTTCATTATTCCTTTGGTATATACGATGTGGCTGA	360		
OY 344	ctgagcgcatcatgtcccttgattggttgttagcataatttgcgacctccatctacagtt	403		
Db 361	TTGGGAGCCAAAGGCCCTTTGACCGCTATATGTGCTATATGTTCGCCACCTACCTATGCAACC	420		
OY 404	atcatgcacacagagactctgcctccagttgcagctgcagctgcatctctggttaactggttaagt	463		
Db 421	CGATGAGTCTGTGGGCTATGTGCTATTGTGGCAATTGTCTATATGGTGATATGGATGCATA	480		
OY 464	aactcagttgtgttcttctacccctgaactctcagctgcagctgcacactctgtaaccctatgata	523		
Db 481	GTAGTCTGGGACAGACCAATTTATTATTTTCCTTTGAAACTCTGTGGACCCCTGTGAGATA	540		
OY 524	gataactctctctgtgaagtcctccgcagctgttcaagttatcttgttgttgaagaacaagca	583		
Db 541	GACCACTTCTTGTGACCTTTCACCTCTCTCTGTGGACACTGTCTTGTGTGGATATATCCAA	600		
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Db 601	AATGAGCTGGCATTCTTGTGTGGACAGAGTCTCTGCAATTATTATTCATTTTTACTGATC	660		
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[illegible]

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? APPLICANT: SUTTON III, GRANGER G.
? APPLICANT: ROSEN, CRAIG A.
? TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
? TITLE OF INVENTION: Coupled Receptor GPR2
? NUMBER OF SEQUENCES: 30
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: STERNER, KESSLER, GOLDSTEIN & FOX P.L.L.C.
? STREET: 1100 NEW YORK AVE., NW, SUITE 600
? CITY: WASHINGTON
? STATE: DC
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: FLOPPY DISK
? COMPUTER: IBM PC COMPATIBLE
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/467,948A
? FILING DATE: 06-JUN-1995
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: PCT/US95/04079
? FILING DATE: 30-MAR-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: STEFFE, ERIC K.
? REGISTRATION NUMBER: 36,688
? REFERENCE/DOCKET NUMBER: 1488..1140003/EKS/KLM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2600
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1713 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 116..1003
? US-08-467-948A-1

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Oy	73 gttccactccttgtgtctctcttgatttcttaacagtggaccatcttggacaatctgac	132			
Db	196 GATGTCCTCTTTGGGCTCTCTCCCTGTTCATGCTTCACGCCGCGGGGAATGGGAC	255			
Oy	133 catctcttagtgcagccctggagaccaaatctatatccccatgatatttttcttac	192			
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Db	316 ACACCTGGCCGCHGCACAACTGGCTATGGCTGCAACAACAGTGGCCCCAGATGCTGTGAA	375			
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Db	376 CCTCCTGCATCCAGCAGACCOCATCTCCTTGCTGGTTGCATGACATAGACTTTCCTT	435			
Oy	313 tctgaccttgaggggatcttgaaatatctctcctcgccgtcaatgtccttgattggtgt	372			
Db	436 TTTGAGTTTTCACATACTGAATGCCCTCTGTTGTCGTGATGTCTTACGATCGGTACGT	495			
Oy	373 agctaattgtcgacctccatacttaactagttatacatagtacacagagaactctgcctcagtc	432			

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Qy	433	ggagagcgcgaatcccgaggttaactggtttagttaactcaagtgtgtgtcgtacccctgactc	452
Db	556	GGGCATCATCTTCGAGACAMGTGGCTCCCTCGGCTATGGTCCAMGTGAGCCCTCATCTCT	615
Qy	493	ccaagtcgcaactcgtgtaaccctatgfatagatcaacttctctgtgaatgccctgact	552
Db	616	AAGACTGCGCTTTGTGGGCGCTCGTGAATCAACCACTTCTCTGTGAATTCCTGTCTGT	675
Qy	553	gctcaagtattctgtgtgtttagacaacagcaaatagagctgtaacttctgtcagtga	612
Db	676	CCTGAGCTGGCCCTGTCTGATATACCTGGCTCAACCAAGTGGTGATCTTTAAAGCTTGCA	735
Qy	613	gctcttcacatcaataccocctgacacccatccatctatcatgatgcttttatgtgcgagc	672
Db	736	GTATATCTGCTGGGACCACTCTGCTGGTGTGTTCTCTACTACACATCTGGGGGG	795
Qy	673	agatattgagatacagtcgtcgtgaagtcgacaanaagcatttggagacatgtgtccca	732
Db	796	CATCCTGAGATCCAGTCTGGGGAGGGCCGAGAAAGCCCTTCCACACGTCTCTCCCA	855
Qy	733	tctaatgtgtgtctcttttttatagtaacgcgcttctgtgttaactgtaaccaacttc	752
Db	856	CCTCTGGTATGTGGACCTCTTCTTTGGSAGCGCATCGCATATGATAGGCCCTTAAGTC	915
Qy	793	gccccagctccaaaggacccaagaagaatgtgttctctctctcatgaaatcatgtgacccat	852
Db	916	CCGCAATCTGAGSAGSAGCAGCAAGAAAGTCTTTTCTTATTTTACAGTTCCTTTCAACCC	975
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Db	976	GATG 979	
RESULT 6			
US-08-467-947A-1			
: Sequence 1, Application US/08467947A			
: Patent No. 6090575			
: GENERAL INFORMATION:			
: APPLICANT: LI, YI			
: APPLICANT: CAO, LITANG			
: APPLICANT: NI, JIAN			
: APPLICANT: GENTZ, REINER			
: APPLICANT: BULF, CAROL J.			
: APPLICANT: SUTTON III, GRANGER G.			
: APPLICANT: ROSEN, CRAIG A.			
: TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein			
: TITLE OF INVENTION: Coupled Receptor GPR1			
: NUMBER OF SEQUENCES: 30			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.			
: STREET: 1100 NEW YORK AVE., NW, SUITE 600			
: CITY: WASHINGTON			
: STATE: DC			
: COUNTRY: USA			
: ZIP: 20005			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: FLOPPY DISK			
: COMPUTER: IBM PC COMPATIBLE			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/467,947A			
: FILING DATE: 06-JUN-1995			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			
: APPLICATION NUMBER: PCT/US95/04079			
: FILING DATE: 30-MAR-1995			
: ATTORNEY/AGENT INFORMATION:			
: NAME: STEFFE, ERIC K.			
: REGISTRATION NUMBER: 36,668			

```

? REFERENCE/DOCKET NUMBER: 1488.1140002/ERK/XLM
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 202-371-2600
? TELEFAX: 202-371-2540
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1713 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: both
? MOLECULE TYPE: CDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 116..1003
? US-08-467-947A-1

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Query Match	21.1%	Score 199.2	DB: 3	Length 1713
Best Local Similarity	52.3%	Pred. No. 2	1e-52	
Matches	441	Conservative	0	Mismatches 403; Indels 0; Gaps 0;
QY	13	aaatlcagacatcaatcacagagatttattctcgtggttcttcagatcagacctgtgcgtga	72	
Db	136	AAATCAGACAAATGTCACAGAGATTCTCTACTGGGATTTCTCCGAGCCCAAGGATTC	195	
QY	73	gtttccactctctgtgtgtctctcttgattcttcaacgtgcgtacatcttggcaatctgac	132	
Db	196	GATGTCCTCTTTTGGGCTCTTCTCCCTGTCTATGCTTTCACCCCTGCGGGGAAAGGAGC	255	
QY	133	catcttctagtgatcagcgtgcagacacaacattcatcccccatgtaattttttctaac	192	
Db	256	CATCCTGGGGGCTCATCTCACTGACACTCCAGACTCCACACCOCACATGTAATCTTCTCTC	315	
QY	193	caatctatcaactcctcgtgactcttgtlttacaccaatgtaacgtlcccaaaatgtagtaa	252	
Db	316	ACACCTGGCCGCGTCACATGCTGCTATGCTCGCAACAGAGGCCCCAGATGCTGTGTA	375	
QY	253	tttaagcagcatcagaaagtaaatagttatcgtgtgcgtgtglaagccagcttttcattt	312	
Db	376	CCTCCTGCATTCAGCCAAAGCCCATCTCCTTGTGCTGTGATGATGACATGACTTCTCTT	435	
QY	313	ctctgaccttgggggactagataatcttctctcgtgcgcgtcaatgtcccttgaattgttgt	372	
Db	436	TTTGAGTTTGGACATACACTGAAATGCTCTGTTGTGCTGTAATGCTCTGATCGGTAGCT	495	
QY	373	agctatttgtgcgctctccatctactacgtatcaatgcacaaagaaactctgcctcagttc	432	
Db	496	GGCCATCTGCGCACCCCTCCCGATATTTATCATCATGACCTGGAAAGCTCATCACTCT	555	
QY	433	ggcagctgcacacccgtgtactcgtgttttagtaacctcagtggtgtgtcttaaccgcacct	492	
Db	556	GGGCAATCACTTCCTGTGACATGTGGCTCCCTCTGCGTATGTGTCATGTGAGCTCTATCT	615	
QY	493	ccagcttgcacactctgtgacccctatgtatagatcatcttctctgtgagccctgcacct	552	
Db	616	AAGACTGGCCCTTTGTGGGCTCGTGGAAATCAACACACTCTTCTGTGTAATTCGTCTGCT	675	
QY	553	gctcaagttatctgtgtgtgtgagacaacagcaaatgaggctgaactatctctgttcagtga	612	
Db	676	CCTCAGGCTGGCGCTGTGATACCTGTGCTCAACCCAGGTGGTCACTTTTGAAGCTGTGAT	735	
QY	613	gctcttcacatcctaataccctcgacacactatccttatcatatgatttttatgttgcagac	672	
Db	736	GTTTCATCTCTGTGGGACCACTCTGCTCTGTGCTGTCTCTACTACACATCTCTGGGGGG	795	
QY	673	agttatcgagatacagtcctgtcgaaggtcgaacaaagacatttgggaaatgtgtgtccca	732	
Db	796	CATCCTGAGGATACAGCTGTGGGAGGGGCCGAGAAAGSCCTTCTCACACCTGCTCTCCCA	855	
QY	733	tctaatgtgtgtgtctcttttttaagtaacagcgctctcgtgttaacctgcaaacaccttc	792	
Db	856	CCTTCGCGCTAAGGGACCTCTTTTGGGAGGGCCGACCTCTCATATGTAACAGGCCCTTAATGC	915	

REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5600
TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-6

Query Match 20.4%; Score 192; DB 3; Length 966;
Best Local Similarity 53.5%; Pred. No. 2.8e-50;
Matches 399; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

164 cttcataccccatgtatctttttcttcaaatcctacatccttgatcttggtaacc 223
181 ctacacacccccctgactcttcttgcacacactgtctcctgcgagatggctatgct 240
224 acatgacagtcac 283
241 tgcctctctac 300
284 cgtgctctgtgac 343
301 gagggagtgccac 360
344 ctggcgctatgctccttgatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 403
361 ttggcaccac 420
404 atcagcaccagac 463
421 cgatgagtgctgac 480
464 aactcagtgctgt 523
481 gtacgtctggac 540
524 gatcactctctgt 583
541 gaccactctgt 600
584 aatgagctgaactatcctgt 643
601 aacgagcctgcac 660
644 ctatatacatgctcttattgt 703
661 ctgtatcttctgt 720
704 caaaaacatttggagacatgt 763
721 catraaacctctttccac 780
764 ggcgtctctgt 823
781 gtgctctgt 840
824 tctctctctatggaatcattgacacacacacacacacacacacacacacacacacacac 883
841 gccctctctgt 900
884 aagagagtaagagagac 909
901 aaggaagtaagagac 926

RESULT 9
US-08-748-506-9

Sequence 9, Application US/08748506
Patent No. 6159707
GENERAL INFORMATION:
APPLICANT: Ronnett et al.
TITLE OF INVENTION: NOVEL SPERM RECEPTORS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Volt & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
City: Chicago
STATE: IL
COUNTRY: US
ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 74940
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5700
TELEFAX: 312-616-5600
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 984 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-748-506-9

Query Match 19.6%; Score 185.2; DB 3; Length 984;
Best Local Similarity 50.7%; Pred. No. 3.7e-48;
Matches 445; Conservative 0; Mismatches 433; Indels 0; Gaps 0;

14 aatgacagcatcaacagagattatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 73
31 aatggagacttggctcgagattcatcttgaggggtraccctgtggccgacacactgaag 90
74 ttccactcctgt 133
91 atccctgt 150
134 atattatgtagtgcacgt 193
151 ataatatgacatcactgt 210
194 aatcatacactcctgt 253
211 accctgt 270
254 ttatgacagcatcaacagagattatctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 313
271 attgtgtgacagagac 330
314 ctggccttggagtgatgaatcctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 373
331 ctgt 390
374 gctattgt 433
391 gccatctgcaaacactgtatattcaaacacatcatgtgagccacacagagatgtgtgtgtgt 450

QY 434 gcagctgacacccggtggtgtaactggttgaactcagctggtgtgtctacccgtaactctc 493
DB 451 GTTACTGTCTGTTTATTTTGGGCTTCTCTTCATGGCCAGTCCAGTTGTGATGCTTTTCC 510
QY 494 cagctgcaactctgtgacccctatgtagatcactctctctgtgagtcctcagctg 553
DB 511 AAGCATTATTACTGTGGTCCAAACATTATTCCTACCTTTTCTGTGATTTTGACCCCTG 570
QY 554 ctcaagttatctgtgttgagacacagcaaatgagctgaactactctgtlcaigtgag 613
DB 571 GCAAAATCTCTGCTGTGAGAAACAGAGCTGATGATGCTGTTTATACCTTGTGTA 630
QY 614 ctcttcacatcaaacaccccgagacatcactctatcatalgatttattgtccagca 673
DB 631 ATGTGTCTTTTGGCTTCTTTTATAGCCATCTTGTGATACAGCAATATATAGTACCC 690
QY 674 gttatgagatagacgtctgtcgaagctgacaaagacattggagatgtgttccat 733
DB 691 ATATGTGAGACTCCCTTATAGCCAGGAGGAGCAGACAGAGCTTTTTCACCTGCTCTCAT 750
QY 734 ctatgtgtgtctctcttttattagtagacagcgctctgtgtacactgcaaccacttcg 793
DB 751 CTGATTTCTCTCTCTCTATATGATGAGCAGCTGTGATTTATATCTGAAGCCAAAGCAG 810
QY 794 cccagctcccaaggaagaaagatgttctctctctctcatgtaacatcgtcaccatg 853
DB 811 AGAAGCAGAGTGGACCAACAGAGAGGCTGCTTGTGAACATGTTGTGACACCCCTT 870
QY 854 ctgaacccttatatacacttagaagaagaagt 891
DB 871 CTGACCCCTGTGATCTACACCTGCGCAACAGCAGGT 908

RESULT 10

US-09-439-313-526
; Sequence 526, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuxu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 526
; LENGTH: 963
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-439-313-526

Query Match 12.7%; Score 120; DB 4; Length 963;
Best Local Similarity 49.1%; Pred. No. 7.9e-28;

Matches 318; Conservative 0; Mismatches 330; Indels 0; Gaps 0;

QY 110 gtaacatcttggcaactgacatattctagtgtacgctcggaaccaatctcat 169
DB 106 gttgcaatgtttggaactgtgtgtcttcatcgtlaaggaagacgacgactgac 165
QY 170 accccatgatttttttctacaatcactactcctgtgactctgtttacacactgtc 229

DB 166 gctccgaltgacctcttctctgcatgctgtgcaagcaattgaactgacctatccacatcc 225
QY 230 acagttcccaacaatgctagtaaatltaagcagctcaggaagaatgaatcagttacgtgac 289
DB 226 accatgcttaagatcccttgccttcttctgtttgattcccgagagatgaactgtgagcc 285
QY 290 tdtgtaagccaagctttcattatctctgtcgttggggctactgaatatctctccgtgcc 349
DB 286 tgtcttccagagatgtcttattcatcagccctcgaagcaattgaatccacactctgtc 345
QY 350 gtcattgctttagttgtgttagatctgtgtgcgctctccatctcaatgatarcatg 409
DB 346 gcatgtgctttagacgttattgtgtgcatctgcaaccactggtccatgtgtcagctc 405
QY 410 caccagaagctctgctccagtttgccagctgcaatccctgtgttactgttttagtaactca 469
DB 406 aacatacagtaaacagccagatgtgacatcggtgtgtgttcgcygatalccctctttt 465
QY 470 gttgtgtgtctacccctgactctccagctgcacactctgtgaacctatgtatagatcac 529
DB 466 ttcccaactgctctgtcgtatcaagcgtgtgctctgcaactcacaatgtctctcgac 525
QY 530 ttctctgtgaagtcctctgcaactgcaatgattactgtgttgagacaagaacaatgag 589
DB 526 tccatgtgttcccaagcagatgtaagatgtgacctatgcaagacattgtgccaatgtg 585
QY 590 gctgaactatctctgtcagtgagctcttccatcaataacccctgaacatcatcattata 649
DB 586 gtaatgtcttactgcatcttctgtctatggtgagcggtgagcgaatgttcatctctct 645
QY 650 tcatatgcttattgtctcagcagcatatgaagatagactgtctgaaggtgcgaaaaa 709
DB 646 tccatttctgataacagcaagcgttctgcaactgcttccaaagtaagagcgagcgaag 705
QY 710 gcatttggagacatgtgttcccatcaatggtgtgtctcttttatt 757
DB 706 gccttggaaacgtgtgtcacaatcgtgtgttactgcttctcat 753

RESULT 11

US-08-465-980-1
; Sequence 1, Application US/08465980
; Patent No. 5756309
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel R.
; APPLICANT: Li, Yi
; APPLICANT: Rosen, Craig A.
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPR4J70
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELIA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; City: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,980
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700


```

; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1474 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 274..1233
; US-08-465-980-1

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Query Match      12.4%; Score 116.8; DB 1; Length 1474;
Best Local Similarity 48.8%; Pred. No. 9.6e-27;
Matches 316; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

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QY 110 gtgacacattcttggaacatcgacattatctagtgtcaagcctggaacacaaattcat 169
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Db 379 gtggcaatgtgtggaacatcgacatgctgttcatcgttaaggagacggaaacgacctgac 438

QY 170 accccatgatttttcttacaatctacacccctgactcttgtaaccacatgt 229
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Db 439 gctccagatgacctgttctctgcatgcttgacacattgacctggccttatccacatcc 498

QY 230 acagtcaccacaatgtcagtaaaattatgacagcatcaagaagaatlaacagtaatcgtgac 289
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 499 accatgacctgaagatccttgcccttctggttgatcccgagagattgacattgagagcc 558

QY 290 tgtgtgacccagcttctacattctgagccttgggggctctgaatacttcctcgcc 349
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Db 559 tgctttaccagatggttcttattcatgccccttcacgacattgaatccacacacacacac 618

QY 350 gtaatgctcttgatgtgtgtgtagctatctgtcgcgctctcactacactacatg 409
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Db 619 gccatggccttggacgcttattggtggccatctgacacacacacacacacacacacac 678

QY 410 caccagagactcgtcctcagctgagcagctgacatccttgggttactggttttagtaactca 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 aacaaatgacatgacagccgacattggcattgctgtgctggcagatccctcttcttttt 738

QY 470 gtgtgtgtgtcaccctgacactccagctgacactgctgagaccctatgtagatcac 529
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Db 739 ttcccacatgctctgtctgacatcagcggcctgttctgcccacttccaaatgctctgcac 798

QY 530 tttctctgtgaagtcctgacactgctcaagctatctgtgtgtgtaagaacaagaacatgag 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 799 tccattgtgtccacacagatgtaataatgagtgccctatgacacacatttggcccaatgac 858

QY 590 gctgaactatctctgtcagtgagctctccactcaataacccctgacatcactcattata 649
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 859 gtaatgagcttactgctgacatttgcgtgcatgagcgtgacgtaaatgattctcctttg 918

QY 650 tcaatgacttattgtcgcagagatagagatagacgtcgtggaagtgtagaataaa 709
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 919 tccattttttgtgtaataacagaggttctgcaactgcttccaaagtcagagcgccgaag 978

QY 710 gcaattggagacatgtgtgtccactcaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 757
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Db 979 gccattggagacatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1026

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```

RESULT 12
; Sequence 1, Application US/09053303
; Patent No. 5948890
; GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel R.
;   APPLICANT: Li, Yi
;   APPLICANT: Rosen, Craig A.
;   APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: HUMAN G-PROTEIN RECEPTOR HPRAL70

```

```

; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,
; ADDRESSEE: STUART & OLSTEIN
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/053,303
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/465,980
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ferraro, Gregory D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-446
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1474 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 274..1233
; US-09-053-303-1

```

```

Query Match      12.4%; Score 116.8; DB 2; Length 1474;
Best Local Similarity 48.8%; Pred. No. 9.6e-27;
Matches 316; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

```

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QY 110 gtgacacattcttggaacatcgacattatctagtgtcaagcctggaacacaaattcat 169
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 379 gtggcaatgtgtggaacatcgacatgctgttcatcgttaaggagacggaaacgacctgac 438

QY 170 accccatgatttttcttacaatctacacccctgactcttgtaaccacatgt 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 439 gctccagatgacctgttctctgcatgcttgacacattgacctggccttatccacatcc 498

QY 230 acagtcaccacaatgtcagtaaaattatgacagcatcaagaagaatlaacagtaatcgtgac 289
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Db 499 accatgacctgaagatccttgcccttctggttgatcccgagagattgacattgagagcc 558

QY 290 tgtgtgacccagcttctacattctgagccttgggggctctgaatacttcctcgcc 349
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Db 559 tgctttaccagatggttcttattcatgccccttcacgacattgtaataccacacacacac 618

QY 350 gctgaactatctctgtcagtgagctctccactcaataacccctgacatcactcattata 649
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Db 619 gccatggccttggacgcttattggtggccatgcccacacacacacacacacacacacac 678

QY 410 caccagagactcgtcctcagctgagcagctgacatccttgggttactggttttagtaactca 469
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 679 aacaaatgacatgacagccgacattggcattgctgtgctggcagatccctcttcttttt 738

QY 470 gtgtgtgtgtcaccctgacactccagctgacactcgtgagaccctatgtagatcac 529
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 739 ttcccacatgctctgtctgacatcagcggcctgttctgcccacttccaaatgctctgcac 798

```


FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSNOT01
CLONE: 364702
US-08-988-876-2

Query Match 10.2%; Score 96; DB 3; Length 1828;
Best Local Similarity 55.7%; Pred. No. 3.2e-20;
Matches 206; Conservative 0; Mismatches 160; Indels 4; Gaps 1;

QY 35 ttatctctgtggttctcgaatcgaaccttgctgagttccactccttggtcttc 94
DB 814 TTCCTCTCTAGAGCTCAGGGGATCAGAACTGCAGCCAGCTGCTGGCTGTTC 873
QY 95 ttgattcttaactgacatcttggaactgacattatctagtgtcaagcctg 154
DB 874 CTGCTCAGTGTGCTGTCAGGCTGCTGGGACTGCTCATCTGCGCATAGCCCT 933
QY 155 gacaccaactcaatacccatgtattttcttcaatactatactccttgatctt 214
DB 934 GACTCCACCTCCACACCCCATGTCTCTCTCTCAACCTGCTGCTGCTGACATC 993
QY 215 tgttaaccacatgttaagtcacaaatgtagtaattatgacgacataagaaagta 274
DB 994 GGTTCACCTCCACACGAGTCCCAAGATGATGTGACATCCAGTCTCAGCAGAGTCC 1053
QY 275 atcagttatgctgctgtgtagccagctttcatatttctgctgggggagctatga- 333
DB 1054 ATCTCCATGACAGCTGCTGCTGACATGATGCTCTCTTTGGCATTTTGGAGGATGAA 1113
QY 334 --atattcttcctggcgtlcatgltccttgaattgttgtagctatttgcgacct 390
DB 1114 GAGAGACATGCTCTGATGTGATGGCTATGACTGGTTGTACCATGTGTCAACCGCT 1173
QY 391 ccattactca 400
DB 1174 ATATCATTTCA 1183

RESULT 15
US-08-599-252-84/c
Sequence 84, Application US/08599252
Patent No. 570343
GENERAL INFORMATION:
APPLICANT: DRAVNA, DENNIS T.
APPLICANT: FEDER, JOHN N.
APPLICANT: GRIKKE, ANDREAS
APPLICANT: KIMMEL, BRUCE E.
APPLICANT: THOMAS, WINSTON J.
APPLICANT: WOLFF, ROGER K.
TITLE OF INVENTION: METHOD TO DIAGNOSE HEREDITARY
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,252
FILING DATE: 09-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 9053-0001.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
TELEX: 90-4030
INFORMATION FOR SEQ ID NO: 84:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-599-252-84

Query Match 9.6%; Score 90.2; DB 1; Length 1320;
Best Local Similarity 65.8%; Pred. No. 1.8e-18;
Matches 131; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 719 acatgtgttccatctaattgtgtgtctcttttataagtaagcgcgtctgtgtac 778
DB 1319 ACTTGACGCTGCATCTATGTGTCTCTCTCTCTATGTGATACATCATATATGATGAC 1260
QY 779 ctgcaaccaccttgcagctccaaggaagaaagatggttctctcttctatgga 838
DB 1259 CTCGAGCCAGCAAAATCTTATTTCCAGGACCAAGGAAATTTCTTCTTACACA 1200
QY 839 atcattgacccatgctgaatcccttatataacttaagaaagaaagaaagaa 898
DB 1199 ATTGTCACTCCAGTGTTAACCCCTGATCTATACATTAAGAAACAAAGATGTTAAAG 1140
QY 899 ggccttaaaaggtggtg 917
DB 1139 GCCATGAAGAAGGTGCTGAG 1121

Search completed: August 25, 2002, 18:57:33
Job time: 4586 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 25, 2002, 13:20:02 ; Search time 1886.27 Seconds

(without alignments)
6747.512 Million cell updates/sec

Title: US-09-800-321a-3

Perfect score: 943
Sequence: 1 tatgaattggtaaatgaaca.....tctcttaatacaagaataaa 943Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estha:*
2: em_esthnu:*
3: em_estlin:*
4: em_estlmu:*
5: em_estloy:*
6: em_estlpl:*
7: em_estro:*
8: em_hnc:*
9: gb_estl:*
10: gb_estl2:*
11: gb_hnc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vtl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	337.4	35.8	479	12	AQ077154 CIT-HSP-2
2	226.6	24.0	2021	11	BC016940 Homo sapi
3	204.6	21.7	523	9	AI604386 vv74c09.x
4	200.2	21.2	692	12	AZ090606 RPT-23-2
5	197.2	20.9	642	12	AZ969227 2M0241J24
6	193.4	20.5	1394	11	AK017036 Mus muscu
7	193.4	20.5	3063	11	AK016560 Mus muscu
8	192.6	20.4	632	12	AZ511623 IM0356C17
9	185.4	19.7	428	10	N68399 zai13b04.s1
10	184	19.5	326	12	AZ694245 AST-2HBG3
11	178.6	18.9	640	12	AZ516219 RPT-11-3
12	177.2	18.8	788	12	BH111304 RPT-24-3
13	176	18.7	853	12	BH331857 CH230-46N
14	175.6	18.6	588	12	AZ413817 IM0188F05
15	173.6	18.4	740	12	AZ607393 IM0429N15
16	165.8	17.6	679	12	AG167722 Pan trogl
17	164.2	17.4	632	12	AZ765752 IM0562E19

C	18	164	17.4	548	12	AZ271125 RPT-23-1
C	19	163.2	17.3	674	12	AG131684 Pan trogl
C	20	159.6	16.9	680	12	AZ709687 RPT-24-8
C	21	156.2	16.6	675	12	AZ396801 IM0161E05
C	22	154.8	16.4	1501	11	AK016338 Mus muscu
C	23	154.2	16.4	522	12	AZ720443 RPT-24-1
C	24	154.2	16.4	660	12	AZ380178 IM0136A04
C	25	154	16.3	686	12	AZ086625 RPT-23-2
C	26	153.8	16.3	534	12	AZ312830 IM0028J19
C	27	153.8	16.3	646	12	AZ638594 IM0498M06
C	28	151.8	16.1	608	12	AZ112932 RPT-23-1
C	29	151	16.0	628	12	AZ977433 2M0253P17
C	30	150.2	15.9	797	12	AZ909618 RPT-24-2
C	31	150	15.9	508	12	AZ373636 IM0126C20
C	32	149.6	15.9	484	12	AQ310400 CITBI-E1-
C	33	149	15.8	639	12	AZ418543 IM0194J10
C	34	148.2	15.7	649	12	BH067870 RPT-24-3
C	35	147.6	15.7	605	12	AZ642411 IM0505I22
C	36	147.4	15.6	532	12	AZ519123 RPT-11-6
C	37	147.2	15.6	553	12	AQ482125 RPT-11-2
C	38	147.2	15.6	614	12	AQ453957 HS_5165_B
C	39	147	15.6	762	10	BG193339 RST12467
C	40	146.8	15.6	680	12	AZ235331 RPT-23-6
C	41	146.4	15.5	534	12	AZ664867 IM0545E05
C	42	146.2	15.5	632	12	AZ382351 IM0154L21
C	43	146.2	15.5	796	10	BG197640 RST17016
C	44	146	15.5	619	9	A1148854 qc70a02.x
C	45	145.8	15.5	678	12	AZ964406 2M0234003

ALIGNMENTS

RESULT 1
LOCUS AQ077154/c
DEFINITION CIT-HSP-2354D1.TF CIT-HSP Homo sapiens genomic clone 2354D1, DNA
sequence.
ACCESSION AQ077154
VERSION AQ077154.1 GI:3438338
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Baas,S., Linher,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
TITLE Use of a Random human BAC End Sequence Database for Sequence-Ready
Map Building
JOURNAL Unpublished (1998)
COMMENT Other.GSS: CIT-HSP-2354D1.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
SOURCE

location/Qualifiers
1..479
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2354D1"
/clone_id="CIT-HSP"
/sex="Male"
/cell_type="Sperm"

BASE COUNT 139 a 100 c 111 g 129 t
 ORIGIN

Query Match 35.8%; Score 337.4; DB 12; Length 479;
 Best Local Similarity 90.9%; Pred. No. 5.8e-81;
 Matches 370; Conservative 0; Mismatches 36; Indels 1; Gaps 1;

538 tgaagccctcctcagctcagctatctctgtgtgagacaacagcaatgagctgaact 597
 Db 479 TGAAGCCCTCCTCTCTGCTCAAGTGTCTGTGTGACACACATGCAATGAGCTGAAGT 420
 598 attcctctcagtgagctctcctcctcctcctcctcctcctcctcctcctcctc 657
 Db 419 ATTCTCATGAGTGTGCTATTCCTTATATCCCGTACACTCAACCTTATATGCTATG 360
 658 ttctatgtcgcagagatattgagagatacagctcgtgagagtcgacaaagcaattgg 717
 Db 359 TTTTATGTTCCACAGCAGTGTGAGATCCACTGCTGACAGCAACAAAGCATTTGG 300
 718 gacatgtgttcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 777
 Db 299 GACATGTGCTCCATCTATATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
 778 cctgcaacacacctcgcagctcagcaagcaagcaagcaagcaagcaagcaagca 837
 Db 239 CCTGCAACACCTTCCACCTGCTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 180
 838 aatcattgcaac 897
 Db 179 AATCATTTGACACCCATGCTGATCCCTTATATATACACTTGTGGAACAAGAGTAAAG 120
 898 aggccttaaaagctgtgtgtgc-aagagctctcctcctcctcctcctcctcctc 943
 Db 119 AGCCTTTAAAGGT 73

RESULT 2
 BC016940 2021 bp mRNA linear HTC 09-NOV-2001
 LOCUS Homo sapiens, similar to olfactory receptor, family 2, subfamily A,
 member 4, clone IMAGE:4424116, mRNA.
 ACCESSION BC016940
 VERSION BC016940.1 GI:16877381
 KEYWORDS HTC.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 2021)
 Strausberg, R.
 Direct Submission
 Submitted (05-NOV-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: gcaps-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome
 Center, Stanford University School of Medicine, Stanford, CA 94305
 Web site: http://www-shgc.stanford.edu
 Contact: (Dickson, Mark) mcdgexill.stanford.edu
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
 R. M.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Series: IRAC plate: 27 Row: 1 Column: 22
 This clone was selected for full length sequencing because it
 passed the following selection criteria: Hexamer frequency ORF
 analysis, Genomescan gene prediction, similarity but not identity
 to protein

This clone has the following problem: frame shifted.

FEATURES
 source Location/Qualifiers
 1. 2021

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4424116"
 /tissue_type="kidney, hypernephroma"
 /clone_lib="NIH_MGC_89"
 /lab_host="DH10B"
 /note="Vector: PCMV-SpOUT6"

BASE COUNT 470 a 546 c 427 g 578 t
 ORIGIN

Query Match 24.0%; Score 226.6; DB 11; Length 2021;
 Best Local Similarity 53.3%; Pred. No. 1.2e-50;
 Matches 478; Conservative 0; Mismatches 419; Indels 0; Gaps 0;

13 aaatgacagcatcacaagagattatctgtgtgttccagatgactgtgtg 72
 Db 437 AAATGACAAATGATGTCACAGAGTCTCTACTGAGATTCTCTGGGCCAAGATTCA 496
 73 gtccacacctctgtgtctctgtatctcctcctcctcctcctcctcctcctcctc 132
 Db 497 GATGCTCTCTTTGGGCTCTTCTCCCTGTCTATGTCTTACCCCTGCGGGGAAATGGAG 556
 133 cattaattagtgtaacgctggaacacacacacacacacacacacacacacacac 192
 Db 557 CATCTGGGGCTCATCTACTGACTCCAGACTCCACCCCATGTACTTCTCTCTC 616
 193 caactatcactcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 252
 Db 617 ACACCTGGCGCTGTCACATGCTGCTATGCTGCAACATGCTGCTGCTGCTGCTG 676
 253 ttatgcagcatcagaagaatcagatcagtcagtcagtcagtcagtcagtcagtc 312
 Db 677 CCTCTGATGATGACCAAGCCATCTCTTGTGCTGCTGCTGCTGCTGCTGCTGCT 736
 313 tctgaccttgaggactcagatcctcctcctcctcctcctcctcctcctcctcct 372
 Db 737 TTTGAGTTTGCACATATGATGATGATGATGATGATGATGATGATGATGATGAT 796
 373 agctattgtgcctcctcctcctcctcctcctcctcctcctcctcctcctcctc 432
 Db 797 GGCCATCTGCAACCTCTCCGATTTTCATATCATATGACCTGGAAAGCTTCATCAT 856
 433 ggcagctgcatcctcctcctcctcctcctcctcctcctcctcctcctcctcct 492
 Db 857 GGCCATCTGCAACCTCTCCGATTTTCATATCATATGACCTGGAAAGCTTCATCAT 916
 493 ccagctgcacactcgtgaacacacacacacacacacacacacacacacacacac 552
 Db 917 AAGACTGCCCTTTGTGTGGGCTCGTGAATCAACCACTTCTCTGTGAATCACTGT 976
 553 gctcaagctatcctcctcctcctcctcctcctcctcctcctcctcctcctcct 612
 Db 977 CCTGAGCTGGCTGT 1036
 613 gctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 672
 Db 1037 GTTCATCTGTGTGGACACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1096
 673 agtattgagatcagctcgtcgaagtcgacaaagcaatcttgagatcgtgttccca 732
 Db 1097 CATCTGAGATCCAGTCTGGGAGGGCCGAGAAAGCCCTTCTCCACCTCTCTCCCA 1156
 733 tctaattgtgtgtcctcttcttcttcttcttcttcttcttcttcttcttcttct 792

QY	DB	1157	CCTGCTAGCTAGTGGACGCTCTTCTTTGGCAGGCCCATGCTCATGTAACAGGCCCTAAGTC	1216
QY	793	gcccgcgcccaaggagaccagaagaatggtttctctctctctatggaatcatgcacccat	852	
DB	1217	CCGGCATCTGTGAGGAGCAGCAAGAGGCTCTTTTCTATTATTACAGTCTCTTTCACACCGCAT	1276	
QY	853	gctgaatcccttatatatatacatcattgaaacaagaaggtaagaagaagcctttaaag	909	
DB	1277	GCTAAACCCCTGTGATTTGCAACCTGAGGAAGTAAGTCAAGGCTCAAGGCTGCCCTGAGAG	1333	
RESULT	3			
LOCUS	A1604386/c	523 bp	mRNA	linear
DEFINITION	vv74c09.x1 Stratagene mouse skin (#937313) Mus musculus CDNA clone			
ACCESSION	IMAGE:1228144	3	similar to SW:0LF2, HUMAN 015062	OLFACATORY
VERSION	RECEPOTR-LIKE PROTEIN FAT1L.			
KEYWORDS	A1604386			
SOURCE	A1604386.1	GI:4613553		
ORGANISM	EST.			
	house mouse.			
	Mus musculus			
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
	1 (bases 1 to 523)			
	Marra,M., Hallier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,			
	Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person			
	,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Rlter			
	,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,			
	Waterston,R. and Wilson,R.			
TITLE	The Mashu-NCI Mouse EST Project 1999			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Marra M/Mashu-NCI Mouse EST Project 1999			
	Washington University School of Medicine			
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA			
	Tel: 314 286 1800			
	Fax: 314 286 1810			
	Email: mouseest@watson.wustl.edu			
	This clone is available royalty-free through LNL; contact the			
	IMAGE Consortium (info@image.lnl.gov) for further information.			
	MGI:653736			
FEATURES	This clone was previously sequenced on the 5' end only, this new			
	data is from the 3' end			
	Possible reversed clone: similarity on wrong strand			
	High quality sequence stop: 457.			
SOURCE	location/Qualifiers			
	1..523			
	/organism="Mus musculus"			
	/strain="C57BL/6"			
	/db_xref="taxon:10090"			
	/clone="IMAGE:1228144"			
	/clone_lib="Stratagene mouse skin (#937313)"			
	/sex="females"			
	/tissue_type="whole skin"			
	/dev_stage="11 weeks old"			
	/lab_host="SOLR (kanamycin resistant)"			
	/note="Organ: skin; Vector: pBluescript SK-; Site:1: EcorI			
	/Site:2: XhoI; Cloned unidirectionally. Primer: Oligo			
	df. Whole skin from 11 week old C57BL/6 female mice.			
	Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5'			
	adaptor sequence: 5' GAATTCGGCGCGG 3' -3' adaptor			
	sequence: 5' CTCGAGCTTTTCTTTTCTTTT 3'			
BASE COUNT	149 a 133 c 150 g 89 t			
ORIGIN	2 others			
Query Match	21.7%;	Score 204.6;	DB 9;	Length 523;
Best Local Similarity	62.2%;	Pred. No. 7.4e-45;		
Matches 321: Conservative	0;	Mismatches 195;	Indels	0;
			Gaps	0;
QY	267	ggaagatcatcgatcatgctgctgtgtagccagcctttcatattctgagccttgaggg	326	
	11111 11111 11111 11111 11111 11111 11111 11111			
DB	516	GAAAGACATACGCTCTTTGAGATCTCTTGTGCACCTTCATCTTCTATCTCGGGGA	457	

QY	327	ctctcgaataltcttcctcgtgcgfcacatgcttccttgattgtttgttgatctattgttcgac	386
QY	387	ctctccattactcaagttcaltcacccagagactctgcctcccaagttggcaactgcatcct	446
Db	456	CGAGGAACTGCAATCCCTGTATGACAGATGAGGCGCTTTGGACCGCTATGTGGCTGTGGCAGC	397
QY	396	ctctccattactcaagttcaltcacccagagactctgcctcccaagttggcaactgcatcct	446
Db	396	CGAGGAACTGCAATCCCTGTATGACAGATGAGGCGCTTTGGACCGCTATGTGGCTGTGGCAGC	397
QY	447	gggttaacttggttttagtaactcaagtggtgtgtgttctaccctgaactctccagctgcacatc	506
Db	336	GGAGCAATGAGGCTGTGAGTGCAGTACAGTTCAGACGCCATTCACACTCTGCGCTGCTTCT	277
QY	507	gtgacctcatgtatagatcactctctctgtgaagtcctccgaactgctaaagtatct	566
Db	276	GTCCCCACCAATCAGGTTGATGACACTTTGTGTGTGAGGTCCCTGTGATTCAGACTGTCT	217
QY	567	gtgttgagacacagacagaaatgagcgtgaactcctctgtcagtgagtcctccatctaa	626
Db	216	GTGGGGACACCAACCATATATAGAAATACAAATGGCATTTGGCAGATGTCTTCAATCTTGGTTG	157
QY	627	taaccctgaacactcactcattatcatatgccttattgttcggagcaagttatggagatc	686
Db	156	TACCTCTGAGGCTCATCTTGTCTTGTATGTTGTCACATGCCAGGGCACTGCTGAGGATTA	97
QY	687	agtcgcgcgaagtgctgcacaaaagatattggagacatgagtcctccatctaatgttggt	746
Db	96	GCTGTGCAAAAGGGGGCGCAGAAAGCTTTTGGAGCTGCTTCCCACTCATATGTGTCA	37
QY	747	ctctttttatagtaacgcgtctcctgtgtaactgc	782
Db	36	CTCTCTCCACAGCTCACTCATCTGTTTATCTC	1
RESULT	4		
LOCUS	AZ090606/c		
DEFINITION	RPCT-23-27B20.TV RPCT-23 Mus musculus genomic clone RPCT-23-27B20,		
ACCESSION	AZ090606		
VERSION	AZ090606.1		
KEYWORDS	GSS.		
SOURCE	house mouse.		
ORGANISM	Mus musculus.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.		
AUTHORS	1 (bases 1 to 692)		
	Zhao, S., Nieman, W., Feldblum, T., Malek, J., Shatsman, S., Akiret, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C. M.		
TITLE	Mouse BAC End Sequences from Library RPCT-23		
JOURNAL	Unpublished (1999)		
COMMENT	Other_GSSs: RPCT-23-27B20.TJ Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCT-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html Plate: 27 row: B column: 20 Seq primer: T7 Class: BAC ends.		
FEATURES			
Source	Location/Qualifiers		
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	/strain="C57BL/6J"		

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/db_xref="taxon:10090"
/clone-"RPCI-23-27B20"
/clone_lib-"RPCI-23"
/sex="Female"
/lab_host="DH10B"
/note="Organ: Kidney/Brain; Vector: PBAC3.6; Site_1:
ECORI; Site_2: EORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EORI and EORI Methylase. Size
selected DNA was cloned into the PBAC3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      205 a      164 c      163 g      160 t
ORIGIN

```

Query Match	21.2%	Score 200.2	DB 12	length 692
Best Local Similarity	58.0%	Pred. No. 1	3e-43	
Matches 374	Conservative 0	Mismatches 268	Indels 3	Gaps 1

Matches 374; Conservative 0; Mismatches 268; Indels 3; Gaps 1;

Oy 279 gttatcgtgacgttggagcccaagctttcatatttcgtgccttgaggagctactgaatc 338
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 692 GCTATGCTGGGTGCATGACCCAGTCTTCATACACACTTTATCGGGTGGAACTAGTG 633

Oy	tctctcgggcgcatatgtcccttgatggtttcttagacatttcggcgccctccacttct	398
Db	632 tectctcttggctgatagccttttcgaccgctantctgcctctgtgtctgcgttcacacttacacacttca	573

Qy 399 cagttacatgaccacagagactctgcctccaaagtctggcagctgcatcccgagctcaactggtt 458
 572 ccagcattatgcacccccctctctcccatgcattggcccatctcctctgggtgggagccc 513

459 ttgattcaactcagctgttggtttgtcttaccctgcgactctccagctcgtgcaactcgttgaccctctg 518
 512 ttgtgacctctctgcactcagacacagctctcattcatctagaccattactctctctgtgtgccatacc 453

Db 452 TGA---ACCACTTCTCTGTGAGATGCTTGTTCCTCCTAAGCGCGCTTGTGAGACACACAG 356

Db 395 TGGGAACAGAGACTACTGTGTTTTGGGCTGGAGCTGTATTTTTGGCTCTGCTCCGTAGCAC 336

Db 335 TAATTCTAAGGCACTATGCACACATTCGTCATCAGCTGTTGAAGATCAAGTCAAGATCTG 276

Db

275	GGCGCAGAAAGCTCTGGGAACCTTGTTGGGTCCACACCTACTACTGTGGTTCCTTTTTCATG	216
-----	--	-----

Db
215 GCTCAGGCATGTACACGATATCTCCAGCCTATCCACAGCATATCTGGTGTGAAGGGAGT 156

Db
155 TTGCTGGCCCTCTTTTATCTATCATTCATCTACTCCATGTCGTAACCTCTGTGATTTATACCCCTAA 96

Db 95 GAAACAAGGATGTAAGGGGCTCTGTGCAGGTACTGTAAAG 51

RESULT	5	
AZ969227		
LOCUS	AZ969227	642 bp
		DNA
		linear
		GSS 37-APR-2001

ACCESSION	AZ9669227	GI:13840454
VERSION	AZ9669227.1	
KEYWORDS	GSS.	

SOURCE	ORGANISM
house mouse.	<i>Mus musculus</i>
	Eukaryota: Metazoa: Chordata: Cranialta: Vertebrata: Euteleostomi;
	Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae; Mus.
REFERENCE	1 (bases 1 to 642)
AUTHORS	Dunn, D., Acyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Dale, M., and M. J. Beatty

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
	Contact: Robert B. Weiss
	weiss@umich.edu

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA
Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0241 row: J column: 24
Seq primer: CACACAGCAACACACTATGACC
Class: plasmid ends
High quality sequence stop: 642.

FEATURES	Location/Qualifiers
source	1. .642

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C2M0241J24"
/clone_lib="Mouse 10kb plasmid U08C2M Library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (g1147321141gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

```

Query Match Similarity	20.9%	Score	197.2	DB	12	Length	642
Best Local Similarity	56.7%	Pred. No.	8	le	43		
Matches 364; Conservative	0	Mismatches	278	Indels	0	Gaps	0

Db 1 TCCCCAGATATGTCGTCATTCTCTGACAGACAGAAATATCTTTTCCATATGAGGCTGTG 60

D6
61 TGACCCAGCCTTTGCATTCAATTTTTTGTGGCTCAGAGTGTCCTCTCGGACGAA 120

Db 121 TGGCATATGATCGATATATTCTCATCTGTGAAGCCGTTAAGGTAAGTCTATTTATTATGACAA 180

ORIGIN				
Query Match 20.5%; Score 193.4; DB 11; Length 1394;				
Best Local Similarity 52.3%; Pred. No. 1,1e-41;				
Matches 428; Conservative 0; Mismatches 381; Indels 0; Gaps 0;				
OY	104	tacacgtgacacatcttggaacatctgacatattcttagtgcagccctggacaccaa	163	
DB	434	TACATGTGGCAGCATGATGACATGAGCTTCTACTCCGTCATCAGACAGTGGATCCGG	493	
OY	164	cttatacccccatgattttttcttaccatatactaccccgatcttctgttaacc	223	
DB	494	CTTACGATACCCATGATACCTCTCTACTGAGCAGCTGTCCTCATTTGACCTCTTCA	553	
OY	224	acatgtacagtcacacaaatgctagtaattatgacagcatcagaagaatcatagtat	283	
DB	554	TCAATTTGAACTCCCAACACAGTGTGGATTTTCTGCTCAGACAGAACACATATCCTT	613	
OY	284	cgtggtcgtgtgtaagccagctttcatatttctggccttgggggactactgaatctctc	343	
DB	614	GAGGAGATGCCCTTCAATTTGTTCTCAGCAATGACATTTGGTGGTGACAGACCTCCTT	673	
OY	344	ctggccctcatgctctttagtattgttgaatattgttgcgctctccatctactagtt	403	
DB	674	CTGGCCTTCAATGACCTTATGATAGTATGTGGCCATTTGTCATCCTTAACTCATGATC	733	
OY	404	atcatgacacagagacatctgctccagttgcaagctgcacatcgtgttactgattagt	463	
DB	734	TTCTATGATCCAAAGGCGCTGCAGGCTCATGTGGCCATATCATGATGATCCTTCTT	793	
OY	464	aactcagttggttgttctacccttaccctccagctgcacatctgtgacccctatgtata	523	
DB	794	AGTCCCTTAGTGCACACAGTGTACCAATGACATTCCTTCTTCCATGTCAGCAAGAAATC	853	
OY	524	gataccttctctgtgaagctccctgcagctgcataatattcttgttggagacaaagca	583	
DB	854	AGACACCTGCTCTGTGAGTCTCTCCATTTGTAATTTGGCTTGTGACAGACATTCACA	913	
OY	584	aatgagcctggaacatctctgtltagtgaagcttctcatataacccctgacatc	643	
DB	914	TATGAGCTCATGTTTATGATGACAGAGATGATTTCTTATGCTCCCTCTGCTCATTT	973	
OY	644	cttatcatatgctttattatgtccgaagcatatgagatacagctgcctgaagctga	703	
DB	974	ATTACCTCTACTACTCAATTAATTTATTCACATGCTGTGCACATGCTTCAAAATGAGG	1033	
OY	704	caaaaacatttggagacatggtgtccacatctaatgtgtgtctcttttattagta	763	
DB	1034	AAGAAACCCCTGTGACCTGTCTCTCCACATGACTGTGTGGATGTTTATGCGGCT	1093	
OY	764	gcgcgtctctgttaccctgcaacacccctgcgcacgtcccaagaccaaagaatggt	823	
DB	1094	GCCACTTTCATATGATGTCGCCACAGTTCTTCCACAGTCTTAAGCAAGACATATCATC	1153	
OY	824	tctctctctatgtaaatcatctgacccaatgtaatcccttatataatacctagaac	883	
DB	1154	TTCTGTGTTTATATACATATTTGACACAGCTCTGAACCCCTCATTTACAGCTGAGAAT	1213	
OY	884	aaggaaggttaaggaagcttaaaaggttggttcaaga	922	
DB	1214	AAGGAGGTGATTTGAGCTGTTAGAAAGACTGCGGAGAG	1252	

RESULT 7
 AK016560 3063 bp mRNA linear HTC 19-JAN-2002
 LOCUS AK016560
 DEFINITION Mus musculus adult male testis cDNA, RIKEN full-length enriched
 library, clone:4932441H21:similar to T1 OLFATORY RECEPTOR, full
 insert sequence.
 ACCESSION AK016560
 VERSION AK016560.1 GI:12855357
 KEYWORDS HTC; CAP trapper.

SOURCE		ORGANISM	
REFERENCE		MUS MUSCULUS (STRAIN:C57BL/6J) ADULT MALE TESTIS CDNA TO mRNA, clone:4932441H21.	
AUTHORS		MUS MUSCULUS	
TITLE		Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
JOURNAL		1 (sites)	
PUBMED		Carninci, P. and Hayashizaki, Y.	
AUTHORS		High-efficiency full-length cDNA cloning	
TITLE		Meth. Enzymol. 303, 19-44 (1999)	
JOURNAL		99279253	
PUBMED		10349636	
AUTHORS		2 (sites)	
TITLE		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	
JOURNAL		Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.	
PUBMED		Normalization and subtraction of cap-trapper-selected cDNAs to	
AUTHORS		prepare full-length cDNA libraries for rapid discovery of new genes	
TITLE		Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL		20499374	
PUBMED		11042159	
AUTHORS		3 (sites)	
TITLE		Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	
JOURNAL		Kono, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,	
PUBMED		Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,	
AUTHORS		Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,	
TITLE		Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,	
JOURNAL		Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J.,	
PUBMED		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, T., and Hayashizaki, Y.	
AUTHORS		RIKEN integrated sequence analysis (RISA) system--384-format	
TITLE		sequencing pipeline with 384 multicapillary sequencer	
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)	
PUBMED		20530913	
AUTHORS		4 (sites)	
TITLE		The RIKEN Genome Exploration Research Group Phase II Team and the	
JOURNAL		FANTOM Consortium.	
PUBMED		Functional annotation of a full-length mouse cDNA collection	
AUTHORS		Nature 409, 685-690 (2001)	
TITLE		5 (bases 1 to 3063)	
JOURNAL		Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,	
PUBMED		Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bull, C.,	
AUTHORS		Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,	
TITLE		Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiroaka, T., Hori, F.,	
JOURNAL		Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Katsukawa, T.,	
PUBMED		Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S.,	
AUTHORS		Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,	
TITLE		Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,	
JOURNAL		Salto, H., Salto, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,	
PUBMED		Shirai, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,	
AUTHORS		Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,	
TITLE		Tanaka, T., Teijima, T., Toya, T., Yamamura, T., Yamana, I.,	
JOURNAL		Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and	
PUBMED		Hayashizaki, Y.	
AUTHORS		Direct Submission	
TITLE		Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of	
JOURNAL		Physical and Chemical Research (RIKEN), Laboratory for Genome	
PUBMED		Exploration Research Group, RIKEN Genomic Sciences Center (GSC),	
AUTHORS		RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,	
TITLE		Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,	
JOURNAL		URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,	
PUBMED		Fax: 81-45-503-9216)	
AUTHORS		Please visit our web site (http://genome.gsc.riken.go.jp/) for	
TITLE		further details.	
JOURNAL		cDNA library was prepared and sequenced in Mouse Genome	
PUBMED		Encyclopedia Project of Genome Exploration Research Group in Riken	
AUTHORS		Genomic Sciences Center and Genome Science Laboratory in Riken.	
TITLE		Division of Experimental Animal Research in Riken contributed to	
JOURNAL		prepare mouse tissues. First strand cDNA was prepared with a primer	
PUBMED		[5' GAGAGAGAGAGAGATCCAGAGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	
AUTHORS		3'], cDNA was	
TITLE		prepared by using trehalose thermo-activated reverse transcriptase	
JOURNAL		and subsequently enriched for full-length by cap-trapper. cDNA went	
PUBMED		through one round of normalization to Rot = 10.0 and subtraction to	
AUTHORS		Rot = 100.0. Second strand cDNA was prepared with the primer	

TITLE , Durick, K. and Pollok, B.
JOURNAL Unpublished tags from a HL-60 Genomescreen(TM) Library
COMMENT Unpublished (2000)
Contact: Greg Henkel
Gene Expression
Aurora Biosciences Corp.
11010 Torreyana Road, San Diego, CA 92121, USA
Tel: 8584048436
Fax: 8584046719
Email: henkel@aurorabio.com

Pools of cells were isolated from a Genomescreen(TM) library. The library of cells was generated by retroviral integration of a gene tagging element consisting of: 1) A promoterless beta-lactamase gene preceded by a splice acceptor as a reporter for gene expression; 2) A promoter driving neomycin resistance followed by a splice donor to trap downstream exons. 3' RACE from neomycin gene was performed using total RNA from isolated pools. Output was shotgun cloned in pAMP-1 and used to transform DH5-alpha competent bacteria. 5' ends of reported sequences were immediately preceded by splice donor from the trapping construct.

Class: exon-trapped.
Location/Qualifiers
1. .326
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Genetrap HL-60 Human Promyelocytic Leukemia Library"
/tissue_type="acute promyelocytic leukemia"
/cell_type="promyeloblast"
/note="Organ: peripheral blood; Vector: pAMP-1; 3' RACE of total RNA from genetrap pools; shotgun clone in pAMP-1 and used to transform DH5-alpha competent bacteria."

BASE COUNT 109 a 65 c 57 g 95 t

ORIGIN

Query Match 19.5%; Score 184; DB 12; Length 326;
Best Local Similarity 100.0%; Pred. No. 2.5e-39;
Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 760 taagacgcgtctctgttgaactgcaacacacgtgcccagctcccaaggaagcaagaagat 819
|||||
Db 1 TACAGCGGTCTCTGTACTGCAACACACCTTCCGCCACGCTCCAGACCAAGAAAGAT 60
|||||

QY 820 gttctctctctctgaatcaltgacccatgctgaatcccttatataactag 879
|||||
Db 61 GGTTCCTCTCTATGGAATGATGCAACCATGCTGAATCCCTTATATACACTTAG 120
|||||

QY 880 gaacaaggaagtaagaaggtcttaaaaggttggtgcaagagctctcttaacaagaa 939
|||||
Db 121 GAACAAAGAGGTAAAGAGAGCTTTAAAGGTTGGTCAAGAGCTCTTAAATCAAGAA 180
|||||

QY 940 ataa 943
|||||

Db 181 ATAA 184

RESULT 11
AZ516219 640 bp DNA linear GSS 16-Oct-2000
LOCUS RPCI-11-350523.TVK RPCI-11 Homo sapiens genomic clone
DEFINITION RPCI-11-350523, DNA sequence.
ACCESSION RPCI-11-350523
VERSION RPCI-11-350523
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 640)
Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter, J.C.

TITLE BAC end sequences of library RPCI-11
JOURNAL Unpublished (1997)
COMMENT Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@delong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genet cs (http://www.tigr.org/tldb/humans/bac_end_search/bac_end_search.html). This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1. .640
/organism="Homo sapiens"
/db_xref="GDB:7634182"
/db_xref="taxon:9606"
/clone_lib="RPCI-11-350523"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPCI11 Human Male BAC library"

BASE COUNT 185 a 99 c 140 g 216 t

ORIGIN

Query Match 18.9%; Score 178.6; DB 12; Length 640;
Best Local Similarity 93.0%; Pred. No. 9.2e-38;
Matches 198; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 732 atctaattggtgtgtctctttatagtagtaagcgtctgttacctgaaccacct 791
|||||
Db 640 ATCTAATTGTGTGTCTCTTTTATGTATGATGATGATGATGATGATGATGATGATGAT 581
|||||

QY 792 cgcacagctccaagaagcaagaagatggttctctcttataagaaatgacacca 851
|||||
Db 580 CACCACGCTCCAAAGACCGGGGAAAGATGTTCTCTCTTGTGGATTCATTCACCCA 521
|||||

QY 852 tgcgaatcccttatataacacttaagaaaggaagtaagaagcttaaaagt 911
|||||
Db 520 TGCTGAATCCCTTATATATACACTTAGAACAAGAGTAAGAACCTTTAAAGCT 461
|||||

QY 912 tggttgc-aagagctctcttaatacaagaataa 943
|||||
Db 460 TGGTTGCAAGAGGTCTCTTATATCAAGAAATAA 428
|||||

RESULT 12
BH11304 788 bp DNA linear GSS 19-Jul-2001
LOCUS RPCI-24-367N6.TU RPCI-24 Mus musculus genomic clone RPCI-24-367N6,
DEFINITION DNA sequence.
ACCESSION BH11304
VERSION BH11304
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Soturognath; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 788)
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akiret, B., Levins, M., Tsengaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)

COMMENT

Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Tel: 301 838 0200
Fax: 301 838 0208
Email: shaying.zhao@broadinstitute.org

Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pdejong@email.cno.org). Clones may be ordered from BACPAC Resources (<http://www.chori.org/bacpac/orderingframe.htm>). BAC end page: http://www.tigr.org/tdb/bac-ends/mouse/bac_end_intro.html

FEATURES	Location/Qualifiers
source	1. .788

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-367N6"
/clone_1lb="RPCI-24"
/sex="Male"

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BASE COUNT	168 a	217 c	162 g	241 t
ORIGIN				

Query Match	18.8%;	Score 177.2;	DB 12;	Length 788;
Best Local Similarity	53.7%;	Pred. No. 2.4e-37;		
Matches 411; Conservative	0;	Mismatches 353;	Indels 2;	Gaps 2;

QY	104	taactctgaccacactcttggaacactgcagcaactatctctaatgtcagccgagacaccaa	163
Db	6	TACATCTTACACCTCGCTCGCAAAATGGAAATATCTTAACTAGTCATCTCCCTGGACCCCAAG	65
QY	164	cttcataaccocccatgtaattttcttctaccaactctacactccctgtaactctgttlaaac	223
Db	66	CTGCACACCCCTATGTAAGTCTTCTTCTTCATATGGCCATTCCTGCATATCTTATGCT	125
QY	224	acatgtaacagtcaccaacaaagtctgaatatttagcagcctcaggaagaatcaagttat	283
Db	126	TTCAACACATGTCCCCAAGATGTGTCCAACTTATTAACAGAAAMAACCAATCTCATTT	185
QY	284	cgtgcctgtgtagccacagcttctcataattctcgtgccttgggagctactgaatactctc	343
Db	186	GCCCAATGCATCACACAGACATCTTGTAATTTGGCCTTTCCGGCTTGGAGTGGTGGATT	245
QY	344	cttgccgctaaagtctcttgatctgttggc- agcatattgtccgagctctcattactcagt	402
Db	246	TTGGCAGCAGATGCTCTATGACAGGTGTGTGGCCATCTGGCACCCCTTACATCACTGTT	305
QY	403	tatactgaccacagagactctgcctccagcttggcagcgtcactcctcgtgtactgctttag	462
Db	306	CATCATGAGTGTGAAGATGTGTGGCCCTGGCTGTCAACATTTGGTCATGTGGATTAG	365
QY	463	taactagtggtgtgtcttactaccctgcgaactctcagctctgcactctgtbaaccctatgcat	522
Db	366	CTCTCTGTGTGCACACACAATTTCTCTGTGAAGTTGCCCTTTGTGTGGCCCAAGGAAT	425
QY	523	agatcacttctctgttgaagtcacctgcactgcactgaatgtactctgtgtttagacaacagc	582
Db	426	AAACACACTCTTCTGTGAATACTGGCTGTCTTCCAACTGGCCGTGGCCGACACTTGGAT	485
QY	583	aaatgagagctgaaactatctctgttctagcttgagcctcttcatactaataccctgaaactca-	641
Db	486	CAACCAATAGCTCATCTAGTGTGATGTGTGTTCGTGTAGTTGGACACCCCTTGTCTTGA	545

Qy	642	tccttatatacagctcttttatctgcagagaaatctgagatacaatctgcgtcaagtc	701
Db	546	tgccttgatcttttacacgcacatcctcttgacaaatcctgaataatcagatcaaaagggtc	605
Qy	702	gacaaaagacatttggagacatgctgtcccatctcaatctgctcttttatagta	761
Db	606	gcaggaaagccctttttccacactgtttccctccatctctgntggtgggctcttttttgta	665
Qy	762	cagccgtctctgttactctgaaccaactctgcgccagctccaagagaccagaagaatgtg	821
Db	666	ttagccatgcttggtttatantgctccctcgatcttgatcaggaagagagcagagaaat	725
Qy	822	ttctctctctcagaaatactgacccatcgtcaatccctcat	867
Db	726	ttttgacctgttccacagactctttttttacccaagaatggaattccctcat	771

RESULT	13
BH331857	
LOCUS	BH331857 853 bp DNA linear GSS 03-DEC-2001
DEFINITION	CH230-46N15.TV CHORI-230 Segment 1 Rattus norvegicus genomic clone
ACCESSION	CH230-46N15, DNA sequence.
VERSION	BH331857
KEYWORDS	BH331857.1 GI:17262571
SOURCE	GSS.
ORGANISM	Norway rat. Rattus norvegicus

FEATURES	Location/Qualifiers
source	1. .853

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/organism="Rattus norvegicus"
/strain="BN/SSNhsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-46N15"
/clone_1id="CHOR1-230 Segment 1"
/sex="Female"
/cell_type="Brain"
/note="Vector: pTARAC2.1; Site_1: EcORI; Site_2: EcORI
CHOR1-230 Rat (BN/SSNhsd/MCW) BAC library produced by
Pietier de Jong"

```

BASE COUNT	210 a	172 c	158 g	313 t
ORIGIN				
Query Match		18.7%;	Score 176;	DB 12; Length 853;
Best Local Similarity		52.4%;	Pred. No. 5.1e-37;	
Matches 409; Conservative		0;	Mismatches 370;	Indels 1; Gaps 1.

Y	108	ctgtgacacatctcttggacatctgacacatcttcttagtctgtaacgcctggaacccaatctc	167
Y	168	ataccccatgtattttcttcttaccacatcatcactccctgattcttggttacaccacat	227
Y	121	ATACACCGATGACTTCTTCATTTCACACTGTCTTTATATGACATCTGTTTATACACCA	180
Y	228	gtacagtcaccaatgctagtaaatatatagaacatcaagaagaataacagtaacgtg	287
Y	181	CCACCATCAACAAAATGTTGGTGAATATTTCAGACTCAATCAATGAGCTTCATTTAGTTATGTAG	240
Y	288	gctgtgtagcccaagcttctcaatattctcgccttgggggctctacgtaatatcttcccg	347
Y	348	ccgtatctccttctgattgattgttagctatttgcggccctccatcattaccagtatca	407
Y	301	TAAATATGCGCTATGATATGTTTGGGCTATCTGTCAATCCACTGAGTACACTGTGCATTA	360
Y	408	tgcaccagaagacatctgcctcagttgtagcagctgcacatccctggttactgtrtttagaact	467
Y	361	TGAATCCCAAAATTCGTGGTGAATGCTTTTGGTTCCTTCATGATAGCAATTTAGATG	420
Y	468	cagtgtagtcttctaccctgactctccagctgcgcactcttgcacccctatgtatagatc	527
Y	421	CTTGTCTCCACACTTTTGATGACGACGCGCCGTCAATTTGACAAAGGTGGAAATTCCTC	480
Y	528	acttctctgtgaagctccctgacatgcgcacagtaattctctgtgtgagacaacagcaatg	587
Y	481	ACTTTTGTGTAAGTACTGCTCAATTTCTCAAGCTTGCAATTTCTCAATTTCTCAATTA	540
Y	588	aggctgaacatctctctgtagtgcagctctccatcctaatacccttgacatcattccta	647
Y	541	ATAATCGTGATTTGGGACAAAGTCTGTTGGGTTCTTCCACTGCTGTATATTT	600
Y	648	tatcatatgctttatttctcgcagcagatattgagagatacagtcgctgaaggtgcacaa	707
Y	601	ATTCTTAATACATGAATTTATTTCTCTGTTGTTGAAATTCATCACTCAGGAAATATTA	660
Y	708	aagcattggggacatgtagtctccatcaattgtagtcttcttcttattagtagacgcg	767
Y	661	AAGTTTCTCCACATGCTCTTACACTTATGATGTTATCTGTTCTATGTTACAGCTT	720
Y	768	tctctgttacctgaaccacacttcgcccagctcccaagaagccaagaagaatggtttctc	827
Y	721	TTGGTGTTATCTGATGTTCTGCTGGCACATCAGACATGAAAGAGTCATATGAGCTCTG	780
Y	828	tctctta-ttggaatcatgacaccatgctgaatcccttatatatatacacttagaacaag	886
Y	781	TGATTTACACTTGTGCTACCTCCATGATGAATCCTTTTATATAGCTTTGACGAATTAAG	840

COMMENT	CONTACT: ROBERT B. WEISS	UNIVERSITY OF UTAH	GENOME CENTER	RM. 308, BIOLOGICAL POLYMERS RESEARCH BLDG., 20 S. 2030 E., SLC, UT 84112, USA	TEL: 801 585 5606	FAX: 801 585 7177	EMAIL: ddm@genetics.utah.edu	INSERT LENGTH: 10000	STD ERROR: 0.00	PLATE: 05	ROW: F	COLUMN: 05	SEQ PRIMER: CGTTGTAAACGACGCGCCACT	CLASS: PLASMID	High quality sequence stop: 588.
FEATURES	Location/Qualifiers														
SOURCE	1..588														
	/organism="Mus musculus"														
	/strain="C57BL/6J"														
	/db_xref="taxon:10090"														
	/clone="U08C1M018F05"														
	/clone_lib="Mouse 10kb plasmid U08C1M library"														
	/sex="Male"														
	/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"														
	/note="Vector: PMD42mv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PMD42 (9114732114[9b]A[129072.1]), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."														
BASE COUNT	157 a 139 c 104 g 188 t														
ORIGIN															
Query Match	18.6%; Score 175.6; DB 12; Length 588;														
Best Local Similarity	66.2%; Pred. No. 5.8e-37;														
Matches 253; Conservative	0; Mismatches 129; Indels 0; Gaps 0;														
QY	32	ggattatctcgtgattctcagatccagcttcgagatcccaactcctgtgctc	91												
DB	198	gaccttcatcctcttctgggattttccagtcgaccccaacttgagacatcatctctcga	257												
QY	92	ttcttgattcttcaactgtgacacatcttctggcaatctgacatattcttagtcaagc	151												
DB	258	gctttgtgcttcttattgtgactctggtaggaacacacacacattatctta	317												
QY	152	ctgagacacaaactcaatcccaatgtatcttttcttaccatctatcaactcctgat	211												
DB	318	ctggagctctccacctccatccatccatgattttcttattcnaattgtcttctgagac	377												
QY	212	ctttttacacacagtacagtcaccacaatgctgaagtaattatctgacacacagga	271												
DB	378	cttctgttattacttactacagcatttccacacagatgctggaatcttcttggggcc	437												
QY	272	gtaacagttacgtgctgtgtgtagccagcttcatcatattctgaccttggggctact	331												
DB	438	tctatttactatgagagggtgtactccagagttcttcttggccctgagactggagac	497												
QY	332	gaatatctcttcctgctgcgtatgctcctttgattgttttagtcatttgtgcctctc	391												
DB	498	gaatgcttcttcttctgctgctgagtgacacacacacacacacacacacacacacac	557												


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Qy      392 cattactcagttatcatgcacc 413
          || || | || | | || || ||
Db      558 CACTACACAGTAATAATGCACC 579
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RESULT	15
AZ607393/c	
LOCUS	740 bp DNA linear GSS 13-DEC-2000
DEFINITION	IM0429N18R Mouse 10kb plasmid U06CIM library Mus musculus genomic clone U06CUM0429N15 R, DNA sequence.
Accession	U06CUM0429N15

BASE COUNT	276 a	134 c	159 g	171 t
ORIGIN				

Query Match	18.4%;	Score 173.6;	DB 12;	Length 740;
Best Local Similarity	54.0%;	Pred. No. 2.2e-36;		
Matches 376;	Conservative 0;	Mismatches 319;	Indels 1;	Gaps 1;

Oy	125	aacgaccattatctcgtgttcaagccctggacacaaactctataccoccatgattc	184
Dd	697	AATCTTGGAAATGATCATTTTATATCAGATGGAATCCACAGCTTCCACACACCAATGTACTTT	638
Oy	185	tctcttaccaatctatcaactccctggatctctgtttacacacatgltacagttcccaaatg	244
Dd	637	TTTTCTACCCACACGCTCTTCTCGAATCTTTGTAATTCACATGCAGTGGCTTAAGATG	578
Oy	245	ctagaaatcttatgcagatctcaagaaagtaactaatgtatcgttgctgttgaocccagctc	304
Dd	577	CTTGTAGACCTACTGCTCTAAGAAATACATCTATTCCTTTCTTGCTGTGCTATGCACTTC	518
Oy	305	tctcaattctctgcccctgtggggccactggaatatctctccctggccgcgcacgtcccttgaat	364
Dd	517	TTCACTTTCTGTATTTTATATAGATGCTGAGTGCTGGCTGGCGACGATGATGGCACTTTGAT	458
Oy	365	tgtgttttagctatattgttcggccctctccatactccagttatcaatgacacagagactctgc	424
Dd	457	CGATATAAGGCCATTATGAAACCCCTTTTGATGTCAGTACATGATCCAGGAAAGTGTGC	398
Oy	425	ctccagttctggcagctgcatactccctggtaactgtgttttagtaactcagctgtgtctacac	484
Dd	397	TTCCATTATATTGACTGGTGTTTATTCTGTGSCATTAGCAGATGCTTTGATATACATACACA	338
Oy	485	ctgactctcagctgccaactctgtgaaccctatgtatagatacacttctctgtgaagtc	544
Dd	337	TTGAAATTCACCAATTATGTTCTGTGGGTCGATAGATATTAATCAATTTCTCTGTGATATT	278
Oy	545	ccctgcacgcgcacagttatctctgtgtttagaacaacaaatgtagctgtgaactctctc	604
Dd	277	CCTCCAGTGTTAGTACTCTCTGTTTCACACACACAGGTCATGTTTATGTCATATTTCACT	218
Oy	605	gtcagttgagctcttccatctaatatccccctgacacttccctatcatatgctttatc	664
Dd	217	GTTTTTGGTTTCATTTGAACCTGAGACCAATCTCAGAGTCTTATCTCTACTGTATATC	158
Oy	665	gtccgagaagatattgagatacagctctgcgttaagtcgacaaaagacatttggaaactgtc	724
Dd	157	ATCTCATGAGTTCTGAAATATGAGTTCTGCTCTCTGGAGGTTAAAAGCTTTCTCTACTGT	98
Oy	725	gatttcccatctcaatgtgtgtctcttctttatagtaacagcgctctctgttactgtcaa	784
Dd	97	ACATACACACGTAGAGTGCTGTTCATTTTTCAGAGCAATATGCTCTTCATGTA-TTCCGG	39
Oy	785	ccaacttgcgccagctccaagaagaccagaagaaagt	820
Dd	38	CCAAAGTTTCTCTACTGCTCCCTAGATCAAGATATAAGTG	3

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